

231870_s_at_HG-U133B	LOC51068	CGI-07 protein	Consensus includes gb:BG291007 /FEA=EST /DB_XREF=gi:13048543 /DB_XREF=est:602386804F1 /CLONE=IMAGE:4515864 /UG=Hs.181022 CGI-07 protein
231873_at_HG-U133B		Homo sapiens cDNA FLJ13364 fis, clone PLACE1000292	Consensus includes gb:AL046696 /FEA=EST /DB_XREF=gi:5434759 /DB_XREF=est:DKFZp434C099_r1 /CLONE=DKFZp434C099 /UG=Hs.315284 Homo sapiens cDNA FLJ13364 fis, clone PLACE1000292
231887_s_at_HG-U133B	KIAA1274	KIAA protein (similar to mouse paladin)	Consensus includes gb:AB033100.1 /DEF=Homo sapiens mRNA for KIAA1274 protein, partial cds. /FEA=mRNA /GEN=KIAA1274 /PROD=KIAA1274 protein /DB_XREF=gi:6331286 /UG=Hs.300646 KIAA protein (similar to mouse paladin)
231897_at_HG-U133B			Consensus includes gb:AL135787 /DEF=Human DNA sequence from clone RP11-16L21 on chromosome 9. Contains the gene for NADP-dependent leukotriene B4 12-hydroxydehydrogenase, the gene for a novel DnaJ domain protein similar to Drosophila, C. elegans and Arabidopsis predicted proteins, t... /FEA=mRNA_1 /DB_XREF=gi:9588110 /UG=Hs.297143 Human DNA sequence from clone RP11-16L21 on chromosome 9. Contains the gene for a NADP-dependent leukotriene B4 12-hydroxydehydrogenase, the gene for a novel DnaJ domain protein similar to Drosophila, C. elegans and Arabidopsis predicted proteins, the GNG10
231926_at_HG-U133B			Consensus includes gb:AK023744.1 /DEF=Homo sapiens cDNA FLJ13682 fis, clone PLACE2000015, weakly similar to EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15. /FEA=mRNA /DB_XREF=gi:10435769 /UG=Hs.318510 Homo sapiens cDNA FLJ13682 fis, clone PLACE2000015, weakly similar to EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15
231945_at_HG-U133B	KIAA1275	KIAA1275 protein	Consensus includes gb:AK001570.1 /DEF=Homo sapiens cDNA FLJ10708 fis, clone NT2RP3000868, weakly similar to Human ovarian cancer downregulated myosin heavy chain homolog mRNA /FEA=mRNA

			/DB_XREF=gi:7022904 /UG=Hs.102796 KIAA1275 protein
			Consensus includes gb:AB037813.1 /DEF=Homo sapiens mRNA for KIAA1392 protein, partial cds. /FEA=mRNA /GEN=KIAA1392 /PROD=KIAA1392 protein /DB_XREF=gi:7243164 /UG=Hs.159200 hypothetical protein DKFZp762K222
231969_at_HG-U133B	DKFZp762K222	hypothetical protein DKFZp762K222	Consensus includes gb:AK001889.1 /DEF=Homo sapiens cDNA FLJ11027 fis, clone PLACE1004114. /FEA=mRNA /DB_XREF=gi:7023437 /UG=Hs.35156 Homo sapiens cDNA FLJ11027 fis, clone PLACE1004114
231981_at_HG-U133B			Consensus includes gb:AF161441.1 /DEF=Homo sapiens HSPC323 mRNA, partial cds. /FEA=mRNA /PROD=HSPC323 /DB_XREF=gi:6841295 /UG=Hs.130714 Homo sapiens HSPC323 mRNA, partial cds
231982_at_HG-U133B			Consensus includes gb:AL049548 /DEF=Human DNA sequence from clone 398G3 on chromosome 6q25.1-25.3. Contains the 3part of the gene for the ortholog of rat CPG2, part of a novel gene, ESTs, STSs and GSSs /FEA=mRNA /DB_XREF=gi:4902741 /UG=Hs.241420 Homo sapiens mRNA for KIAA1756 protein, partial cds
232027_at_HG-U133B			Consensus includes gb:BE740761 /FEA=EST /DB_XREF=gi:10154753 /DB_XREF=est:601593557F1 /CLONE=IMAGE:3947415 /UG=Hs.93758 H4 histone family, member H
232035_at_HG-U133B	H4FH	H4 histone family, member H	Consensus includes gb:AK000776.1 /DEF=Homo sapiens cDNA FLJ20769 fis, clone COL06674. /FEA=mRNA /DB_XREF=gi:7021073 /UG=Hs.128753 Homo sapiens cDNA FLJ20769 fis, clone COL06674
232060_at_HG-U133B			Consensus includes gb:AL390186.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434N1131 (from clone DKFZp434N1131). /FEA=mRNA /GEN=DKFZp434N1131 /PROD=hypothetical protein /DB_XREF=gi:9368899 /UG=Hs.8707 KIAA1301 protein
232080_at_HG-U133B	KIAA1301	KIAA1301 protein	Consensus includes gb:AW504453 /FEA=EST /DB_XREF=gi:7142120 /DB_XREF=est:U1HF-BNO-alq-c-04-0-U1.r1 /CLONE=IMAGE:3080431
232112_at_HG-U133B		ESTs, Weakly similar to KIAA0351 [H.sapiens]	



			<p>/UG=Hs.220745 Human DNA sequence from clone RP4-595C2 on chromosome 1q24.1-25.3 Contains ESTs, STSs and GSSs. Contains the 3 part of the gene for two isoforms of the KIAA0351 protein and the gene for angiopoietin Y1</p>
232125_at_HG-U133B			<p>Consensus includes gb:AU147419 /FEA=EST /DB_XREF=gi:11008940 /DB_XREF=est:AU147419 /CLONE=MAMMA1000616 /UG=Hs.202577 Homo sapiens cDNA FLJ12166 fis, clone MAMMA1000616</p>
232127_at_HG-U133B			<p>Consensus includes gb:AK021494.1 /DEF=Homo sapiens cDNA FLJ11432 fis, clone HEMBA1001099. /FEA=mRNA /DB_XREF=gi:10432689 /UG=Hs.166486 Homo sapiens cDNA FLJ11432 fis, clone HEMBA1001099</p>
			<p>Consensus includes gb:BC004940.1 /DEF=Homo sapiens, Similar to RIKEN cDNA 2210403L10 gene, clone IMAGE:3609702, mRNA, partial cds. /FEA=mRNA /PROD=Similar to RIKEN cDNA 2210403L10 gene /DB_XREF=gi:13436292 /UG=Hs.240951 Homo sapiens, Similar to RIKEN cDNA 2210403L10 gene, clone IMAGE:3609702, mRNA, partial cds</p>
232201_at_HG-U133B	NKD2		<p>Consensus includes gb:AF208502.1 /DEF=Homo sapiens early B-cell transcription factor (EBF) mRNA, partial cds. /FEA=mRNA /GEN=EBF /PROD=early B-cell transcription factor /DB_XREF=gi:6630993 /UG=Hs.185708 early B-cell factor</p>
232204_at_HG-U133B	EBF		<p>Consensus includes gb:AU146384 /FEA=EST /DB_XREF=gi:11007905 /DB_XREF=est:AU146384 /CLONE=HEMBB1000335 /UG=Hs.206868 Homo sapiens cDNA FLJ14056 fis, clone HEMBB1000335</p>
232210_at_HG-U133B			<p>Consensus includes gb:AL353944.1 /DEF=Homo sapiens mRNA; cDNA DKFZp761J1112 (from clone DKFZp761J1112). /FEA=mRNA /DB_XREF=gi:7669984 /UG=Hs.50115 Homo sapiens mRNA; cDNA DKFZp761J1112 (from clone DKFZp761J1112)</p>
232231_at_HG-U133B			<p>Consensus includes gb:AA305476 /FEA=EST /DB_XREF=gi:1957823 /DB_XREF=est:EST176483 /UG=Hs.184062 putative Rab5-interacting protein</p>
232234_at_HG-U133B	C20orf24		<p>chromosome 20 open reading frame 24</p>

232614_at_HG-U133B		Homo sapiens cDNA FLJ12049 fis, clone HEMBB1001996	Consensus includes gb:AU146963 /FEA=EST /DB_XREF=gi:1108484 /DB_XREF=est:AU146963 /CLONE=HEMBB1001996 /UG=Hs.171395 Homo sapiens cDNA FLJ12049 fis, clone HEMBB1001996
			Consensus includes gb:AL080239 /DEF=Human DNA sequence from clone GS1-256O22 on chromosome Xq26.3-28 Contains part of a gene similar to IGFALS (insulin-like growth factor binding protein, acid labile subunit), an EST, STSs, GSSs and a CpG Island /FEA=CDS /DB_XREF=gi:5531259 /UG=Hs.272284 Human DNA sequence from clone GS1-256O22 on chromosome Xq26.3-28 Contains part of a gene similar to IGFALS (insulin-like growth factor binding protein, acid labile subunit), an EST, STSs, GSSs and a CpG Island
232636_at_HG-U133B			Consensus includes gb:AC004908 /DEF=Homo sapiens PAC clone RP5-855D21 /FEA=CDS_3 /DB_XREF=gi:4156179 /UG=Hs.249181 Homo sapiens PAC clone RP5-855D21
232641_at_HG-U133B			Consensus includes gb:AK025419.1 /DEF=Homo sapiens cDNA: FLJ21766 fis, clone COLF7179. /FEA=mrna /DB_XREF=gi:10437927 /UG=Hs.318722 Homo sapiens cDNA: FLJ21766 fis, clone COLF7179
232739_at_HG-U133B			Consensus includes gb:AK026750.1 /DEF=Homo sapiens cDNA: FLJ23097 fis, clone LNG07418. /FEA=mrna /DB_XREF=gi:10439673 /UG=Hs.152432 Homo sapiens cDNA: FLJ23097 fis, clone LNG07418
232841_at_HG-U133B			Consensus includes gb:AB040890.1 /DEF=Homo sapiens mRNA for KIAA1457 protein, partial cds. /FEA=mrna /GEN=KIAA1457 /PROD=KIAA1457 protein /DB_XREF=gi:7959174 /UG=Hs.272759 KIAA1457 protein
232950_s_at_HG-U133B	NIR3	PYK2 N-terminal domain-interacting receptor 3	Consensus includes gb:AI348745 /FEA=EST /DB_XREF=gi:4085951 /DB_XREF=est:ta92e12.x2 /CLONE=IMAGE:2051566 /UG=Hs.163642 Homo sapiens clone 25187 and 25188 mRNA sequences, partial cds
233072_at_HG-U133B	KIAA1857	netrin G2	Consensus includes gb:AU148054 /FEA=EST /DB_XREF=gi:11009575
233106_at_HG-U133B		Homo sapiens cDNA FLJ12375 fis, clone	

		MAMMA1002475	/DB_XREF=est:AU148054 /CLONE=MAMMA1002475 /UG=Hs.288797 Homo sapiens cDNA FLJ12375 fis, clone MAMMA1002475
233137_at_HG-U133B			Consensus includes gb:AF143887.1 /DEF=Homo sapiens clone IMAGE:121687 mRNA sequence. /FEA=mRNA /DB_XREF=gi:4895032 /UG=Hs.18119 Homo sapiens clone IMAGE:121687 mRNA sequence
233138_at_HG-U133B		Homo sapiens cDNA FLJ13412 fis, clone PLACE1001745	Consensus includes gb:AU155968 /FEA=EST /DB_XREF=gi:11017489 /DB_XREF=est:AU155968 /CLONE=PLACE1001745 /UG=Hs.178533 Homo sapiens cDNA FLJ13412 fis, clone PLACE1001745
233177_s_at_HG-U133B	KIAA1184	KIAA1184 protein	Consensus includes gb:AB033010.1 /DEF=Homo sapiens mRNA for KIAA1184 protein, partial cds. /FEA=mRNA /GEN=KIAA1184 /PROD=KIAA1184 protein /DB_XREF=gi:6330254- /UG=Hs.100747 KIAA1184 protein
233195_at_HG-U133B			Consensus includes gb:AL117535.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434F062 (from clone DKFZp434F062). /FEA=mRNA /DB_XREF=gi:5912064 /UG=Hs.150874 Homo sapiens mRNA; cDNA DKFZp434F062 (from clone DKFZp434F062)
233261_at_HG-U133B		Homo sapiens cDNA FLJ11741 fis, clone HEMBA1005506	Consensus includes gb:AU145682 /FEA=EST /DB_XREF=gi:11007203 /DB_XREF=est:AU145682 /CLONE=HEMBA1005506 /UG=Hs.293916 Homo sapiens cDNA FLJ11741 fis, clone HEMBA1005506
233328_x_at_HG-U133B			Consensus includes gb:AL121673 /DEF=Human DNA sequence from clone RP11-305P22 on chromosome 20 Contains ESTs, STSs, GSSs and 7 CpG islands. Contains three novel genes and a novel gene for a helix-loop-helix DNA binding protein /FEA=mRNA_7 /DB_XREF=gi:9650752 /UG=Hs.34487 hypothetical protein FLJ23412
233483_at_HG-U133B		Homo sapiens mRNA for FLJ00050 protein, partial cds	Consensus includes gb:AK024458.1 /DEF=Homo sapiens mRNA for FLJ00050 protein, partial cds. /FEA=mRNA /GEN=FLJ00050 /PROD=FLJ00050 protein /DB_XREF=gi:10440429 /UG=Hs.193857 Homo sapiens mRNA for FLJ00050 protein, partial cds

233500_x_at_HG-U133B	LLT1	lectin-like NK cell receptor	Consensus includes gb:AF285089.1 /DEF=Homo sapiens clone 7B C-type lectin (CLAX) mRNA, partial cds. /FEA=mRNA /GEN=CLAX /PROD=C-type lectin /DB_XREF=gi:9837291 /UG=Hs.136748 lectin-like NK cell receptor
233520_s_at_HG-U133B			Consensus includes gb:AL359338.1 /DEF=Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 2068071. /FEA=mRNA /DB_XREF=gi:8574097 /UG=Hs.50794 Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 2068071
233555_s_at_HG-U133B			Consensus includes gb:AL034418 /DEF=Human DNA sequence from clone RP5-1049G16 on chromosome 20q12-13.2. Contains the 3 end of the NCOA3 gene for nuclear receptor coactivator 3 (thyroid hormone receptor activator molecule TRAM-1, Receptor-Associated Coactivator RAC3, Amplified In Br... /FEA=mRNA_4 /DB_XREF=gi:11546048 /UG=Hs.43857 similar to glucosamine-6-sulfatases
233559_s_at_HG-U133B	FENS-1	phosphoinositide-binding protein SR1	Consensus includes gb:AK023415.1 /DEF=Homo sapiens cDNA FLJ13353 fis, clone OVARC1002182, weakly similar to BETA-TRCP (BETA-TRANSDUCIN REPEAT-CONTAINING PROTEIN). /FEA=mRNA /DB_XREF=gi:10435344 /UG=Hs.44743 KIAA1435 protein
233589_x_at_HG-U133B			Consensus includes gb:AK000392.1 /DEF=Homo sapiens cDNA FLJ20385 fis, clone KAlA4085. /FEA=mRNA /DB_XREF=gi:7020451 /UG=Hs.169758 hypothetical protein FLJ20245
233613_x_at_HG-U133B		Homo sapiens cDNA FLJ13436 fis, clone PLACE1002598, weakly similar to OLIGORIBONUCLEASE (EC 3.1.--)	Consensus includes gb:AU156209 /FEA=EST /DB_XREF=gi:11017730 /DB_XREF=est:AU156209 /CLONE=PLACE1002598 /UG=Hs.296737 Homo sapiens cDNA FLJ13436 fis, clone PLACE1002598, weakly similar to OLIGORIBONUCLEASE (EC 3.1.--)
233813_at_HG-U133B			Consensus includes gb:AK026900.1 /DEF=Homo sapiens cDNA: FLJ23247 fis, clone COL03425. /FEA=mRNA /DB_XREF=gi:10439867 /UG=Hs.288651 Homo sapiens cDNA: FLJ23247 fis, clone COL03425
233845_at_HG-U133B		Homo sapiens clone HQ0452 PRO0452	Consensus includes gb:AF090925.1 /DEF=Homo sapiens clone HQ0452

		mRNA, partial cds	PRO0452 mRNA, partial cds. /FEA=mRNA /PROD=PRO0452 /DB_XREF=gi:6690216 /UG=Hs.283921 Homo sapiens clone HQ0452 PRO0452 mRNA, partial cds
233955_x_at_HG-U133B	HSPC195	hypothetical protein HSPC195	Consensus includes gb:AK001782.1 /DEF=Homo sapiens cDNA FLJ10920 fis, clone OVARC1000384. /FEA=mRNA /DB_XREF=gi:7023268 /UG=Hs.15093 hypothetical protein
234005_x_at_HG-U133B	STK36	serine/threonine kinase 36 (fused homolog, Drosophila)	Consensus includes gb:AK022692.1 /DEF=Homo sapiens cDNA FLJ12630 fis, clone NT2RM4001836. /FEA=mRNA /DB_XREF=gi:10434236 /UG=Hs.26996 KIAA1278 protein
234032_at_HG-U133B			Consensus includes gb:AF119847.1 /DEF=Homo sapiens PRO1550 mRNA, partial cds. /FEA=mRNA /PROD=PRO1550 /DB_XREF=gi:7770130 /UG=Hs.283940 Homo sapiens PRO1550 mRNA, partial cds
234107_s_at_HG-U133B			Consensus includes gb:AL121780 /DEF=Human DNA sequence from clone RP11-555E18 on chromosome 20 Contains the 3 end of the gene for a novel protein similar to bacterial histidyl-tRNA synthetase, ESTs, STSs and GSSs /FEA=mRNA /DB_XREF=gi:10334636 /UG=Hs.306024 FK508-binding protein 3 (25kD)
234132_at_HG-U133B			Consensus includes gb:AK021831.1 /DEF=Homo sapiens cDNA FLJ11769 fis, clone HEMBA1005755. /FEA=mRNA /DB_XREF=gi:10433098 /UG=Hs.306614 Homo sapiens cDNA FLJ11769 fis, clone HEMBA1005755
234140_s_at_HG-U133B	STIM2	stromal interaction molecule 2	Consensus includes gb:AK023369.1 /DEF=Homo sapiens cDNA FLJ13307 fis, clone OVARC1001419, weakly similar to Homo sapiens GOK (STIM1) mRNA. /FEA=mRNA /DB_XREF=gi:10435274 /UG=Hs.306644 Homo sapiens cDNA FLJ13307 fis, clone OVARC1001419, weakly similar to Homo sapiens GOK (STIM1) mRNA
234362_s_at_HG-U133B	CTLA4	cytotoxic T-lymphocyte-associated protein 4	Consensus includes gb:U90273.1 /DEF=Homo sapiens CTLA-4 mRNA, partial cds. /FEA=mRNA /GEN=CTLA-4 /PROD=CTLA-4 /DB_XREF=gi:4099840 /UG=Hs.247824 cytotoxic T-lymphocyte-associated protein 4

234584_s_at_HG-U133B	ATE1	arginyltransferase 1	Consensus includes gb:AF079098.1 /DEF=Homo sapiens arginine-tRNA-protein transferase 1-1p (ATE1) mRNA, alternatively spliced product, partial cds. /FEA=mRNA /GEN=ATE1 /PROD=arginine-tRNA-protein transferase 1-1p /DB_XREF=gi:3808093 /UG=Hs.301497 arginyltransferase 1
234643_x_at_HG-U133B			Consensus includes gb:AK025451.1 /DEF=Homo sapiens cDNA: FLJ21798 fis, clone HEP00573. /FEA=mRNA /DB_XREF=gi:10437968 /UG=Hs.306812 Homo sapiens cDNA: FLJ21798 fis, clone HEP00573
234660_s_at_HG-U133B	DIS3	mitotic control protein dis3 homolog	Consensus includes gb:AL080158.1 /DEF=Homo sapiens mRNA; cDNA DKFZp434L194 (from clone DKFZp434L194); partial cds. /FEA=mRNA /GEN=DKFZp434L194 /PROD=hypothetical protein /DB_XREF=gi:5262618 /UG=Hs.323346 KIAA1008 protein
234682_at_HG-U133B			Consensus includes gb:AL079341 /DEF=Human DNA sequence from clone RP1-319M7 on chromosome 6p21.1-21.3 Contains a gene for a protein similar to KIAA0952 protein, a novel pseudogene, STSs, GSSs and a CpG island /FEA=CDS /DB_XREF=gi:8655533 /UG=Hs.307123 Human DNA sequence from clone RP1-319M7 on chromosome 6p21.1-21.3 Contains a gene for a protein similar to KIAA0952 protein, a novel pseudogene, STSs, GSSs and a CpG island
234725_s_at_HG-U133B	SEMA4B	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B	Consensus includes gb:AK026133.1 /DEF=Homo sapiens cDNA: FLJ22480 fis, clone HRC10841. /FEA=mRNA /DB_XREF=gi:10436886 /UG=Hs.9598 hypothetical protein from EUROIMAGE 1955967
234726_s_at_HG-U133B			Consensus includes gb:AK025482.1 /DEF=Homo sapiens cDNA: FLJ21829 fis, clone HEP01461. /FEA=mRNA /DB_XREF=gi:10438011 /UG=Hs.79353 hypothetical protein FLJ13576
234764_x_at_HG-U133B			Consensus includes gb:U96394.1 /DEF=Human anti-streptococcal anti-myosin immunoglobulin lambda light chain variable region mRNA, partial cds. /FEA=mRNA /PROD=anti-streptococcal anti-myosin immunoglobulin lambda light

			chain variable region /DB_XREF=gi:2352087 /UG=Hs.307341 Human anti-streptococcal anti-myosin immunoglobulin lambda light chain variable region mRNA, partial cds
234839_at_HG-U133B			Consensus includes gb:AL049277.1 /DEF=Homo sapiens mRNA; cDNA DKFZp5641103 (from clone DKFZp5641103). /FEA=mRNA /DB_XREF=gi:4500031 /UG=Hs.274502 Homo sapiens mRNA; cDNA DKFZp5641103 (from clone DKFZp5641103)
234862_at_HG-U133B			Consensus includes gb:AL096770 /DEF=Human DNA sequence from clone RP11-150A6 on chromosome 6. Contains four genes for novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor like) proteins, a DDX6 (DEADH (Asp-Glu-Ala-AspHis) box polypeptide 6 (RNA helicase, 54kD)) ps.. /FEA=CDS_3 /DB_XREF=gi:10198644 /UG=Hs.272282 Human DNA sequence from clone RP11-150A6 on chromosome 6. Contains four genes for novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor like) proteins, a DDX6 (DEADH (Asp-Glu-Ala-AspHis) box polypeptide 6 (RNA helicase, 54kD)) pseudogene
235023_at_HG-U133B		Homo sapiens cDNA FLJ32182 fis, clone PLACE6001823	Consensus includes gb:AA828371 /FEA=EST /DB_XREF=gi:2901470 /DB_XREF=est:ob60g12.s1 /CLONE=IMAGE:1335814 /UG=Hs.292896 ESTs
235051_at_HG-U133B		Homo sapiens cDNA FLJ31090 fis, clone IMR321000102	Consensus includes gb:BF696931 /FEA=EST /DB_XREF=gi:11982339 /DB_XREF=est:602129695F1 /CLONE=IMAGE:4286422 /UG=Hs.55098 ESTs
235052_at_HG-U133B		ESTs, Weakly similar to I38598 zinc finger protein ZNF132 [H.sapiens]	Consensus includes gb:AV758821 /FEA=EST /DB_XREF=gi:10916669 /DB_XREF=est:AV758821 /CLONE=BMFAWC02 /UG=Hs.50405 ESTs, Weakly similar to Z132_HUMAN ZINC FINGER PROTEIN 13 H.sapiens
235061_at_HG-U133B		Homo sapiens cDNA FLJ30116 fis, clone BRACE1000042, weakly similar to PROTEIN PHOSPHATASE 2C ABI2 (EC 3.1.3.16)	Consensus includes gb:AV706522 /FEA=EST /DB_XREF=gi:10723801 /DB_XREF=est:AV706522 /CLONE=ADBDADF07 /UG=Hs.291000 ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
235101_at_HG-U133B	KIAA1014	KIAA1014 protein	Consensus includes gb:AV683244 /FEA=EST /DB_XREF=gi:10285107

			/DB_XREF=est:AV683244 /CLONE=GKCASH01 /UG=Hs.195602 ESTs
			Consensus includes gb:BE502930 /FEA=EST /DB_XREF=gi:9705338 /DB_XREF=est:h21c07.x1 /CLONE=IMAGE:3214380 /UG=Hs.153400 ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
235124_at_HG-U133B			Consensus includes gb:AA398590 /FEA=EST /DB_XREF=gi:2051832 /DB_XREF=est:z75b06.s1 /CLONE=IMAGE:728147 /UG=Hs.97415 ESTs, Weakly similar to E04F6.2 gene product C.elegans
235259_at_HG-U133B			Consensus includes gb:BF530545 /FEA=EST /DB_XREF=gi:11617908 /DB_XREF=est:602071803F1 /CLONE=IMAGE:4214760 /UG=Hs.271853 ESTs, Moderately similar to ALU2_HUMAN ALU SUBFAMILY SB SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
235263_at_HG-U133B	DKFZP434A0131	DKFZP434A0131 protein	ESTs, Weakly similar to JC5314 CDC28/cdc2-like kinase associating arginine-serine cyclophilin [H.sapiens]
235278_at_HG-U133B			Consensus includes gb:AW192700 /FEA=EST /DB_XREF=gi:6471399 /DB_XREF=est:x148h09.x1 /CLONE=IMAGE:2677985 /UG=Hs.253015 ESTs
235287_at_HG-U133B		Homo sapiens cDNA FLJ31360 fis, clone MESAN2000572	Consensus includes gb:BE875232 /FEA=EST /DB_XREF=gi:10324008 /DB_XREF=est:601488533F1 /CLONE=IMAGE:3890600 /UG=Hs.268180 ESTs
235291_s_at_HG-U133B		Homo sapiens cDNA FLJ32255 fis, clone PROST1000226	Consensus includes gb:AI341142 /FEA=EST /DB_XREF=gi:4078069 /DB_XREF=est:qx89e09.x1 /CLONE=IMAGE:2009704 /UG=Hs.197484 ESTs
235331_x_at_HG-U133B		ESTs, Weakly similar to JC4296 ring finger protein - fruit fly [D.melanogaster]	Consensus includes gb:AI887866 /FEA=EST /DB_XREF=gi:5593030 /DB_XREF=est:tk05c07.x1 /CLONE=IMAGE:2150124 /UG=Hs.127335 ESTs
235353_at_HG-U133B	KIAA0746	KIAA0746 protein	Consensus includes gb:AA534416 /FEA=EST /DB_XREF=gi:2278669 /DB_XREF=est:nf76c11.s1 /CLONE=IMAGE:925844 /UG=Hs.162185 ESTs
235359_at_HG-U133B		ESTs, Weakly similar to S42799 gap precursor [H.sapiens]	Consensus includes gb:AW575245 /FEA=EST /DB_XREF=gi:7246784 /DB_XREF=est:UI-HF-BK0-aaw-h-09-Q-UI.s1 /CLONE=IMAGE:3055360 /UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma H.sapiens
235372_at_HG-U133B	FREB	Fc receptor homolog expressed in B cells	



235385_at_HG-U133B	FLJ20668	hypothetical protein FLJ20668	Consensus includes gb:A1935334 /FEA=EST /DB_XREF=gi:5674204 /DB_XREF=est:wo82b12.x1 /CLONE=IMAGE:2461823 /UG=Hs.122406 ESTs
235400_at_HG-U133B	FREB	Fc receptor homolog expressed in B cells	Consensus includes gb:AL560266 /FEA=EST /DB_XREF=gi:12905564 /DB_XREF=est:AL560266 /CLONE=CSODG007YG20 (5 prime) /UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma H.sapiens
235401_s_at_HG-U133B	FREB	Fc receptor homolog expressed in B cells	Consensus includes gb:AL560266 /FEA=EST /DB_XREF=gi:12905564 /DB_XREF=est:AL560266 /CLONE=CSODG007YG20 (5 prime) /UG=Hs.266331 ESTs, Weakly similar to A39878 Fc gamma H.sapiens
235414_at_HG-U133B		ESTs, Weakly similar to S47072 finger protein HZF10, Krueppel-related [H.sapiens]	Consensus includes gb:BF432571 /FEA=EST /DB_XREF=gi:11444722 /DB_XREF=est:nac56h08.x1 /CLONE=IMAGE:3406695 /UG=Hs.164102 ESTs, Moderately similar to S47072 finger protein HZF10, Krueppel-related H.sapiens
235421_at_HG-U133B		ESTs, Moderately similar to ZN91_HUMAN ZINC FINGER PROTEIN 91 [H.sapiens]	Consensus includes gb:AV713062 /FEA=EST /DB_XREF=gi:10732381 /DB_XREF=est:AV713062 /CLONE=DCAADD12 /UG=Hs.122431 ESTs
235422_at_HG-U133B	FALZ	fetal Alzheimer antigen	Consensus includes gb:AA977218 /FEA=EST /DB_XREF=gi:3154664 /DB_XREF=est:oa25h05.s1 /CLONE=IMAGE:1587417 /UG=Hs.118142 ESTs
235428_at_HG-U133B		ESTs	Consensus includes gb:H78106 /FEA=EST /DB_XREF=gi:1056195 /DB_XREF=est:yu83g09.s1 /CLONE=IMAGE:240448 /UG=Hs.104480 ESTs
235444_at_HG-U133B		ESTs	Consensus includes gb:A417897 /FEA=EST /DB_XREF=gi:4261401 /DB_XREF=est:tg55b06.x1 /CLONE=IMAGE:2112659 /UG=Hs.235860 ESTs
235446_at_HG-U133B		ESTs	Consensus includes gb:AW856618 /FEA=EST /DB_XREF=gi:7952311 /DB_XREF=est:RC3-CT0297-060100-012-e08 /UG=Hs.293702 ESTs
235449_at_HG-U133B		ESTs	Consensus includes gb:BF114745 /FEA=EST /DB_XREF=gi:10984221 /DB_XREF=est:7j66h07.x1 /CLONE=IMAGE:3391453 /UG=Hs.136316 ESTs
235459_at_HG-U133B		ESTs	Consensus includes gb:AA858058 /FEA=EST /DB_XREF=gi:2946360 /DB_XREF=est:ob14a03.s1 /CLONE=IMAGE:1323628 /UG=Hs.180711 ESTs
235483_at_HG-U133B		Homo sapiens cDNA FLJ30906 fis, clone FEBRA2006055	Consensus includes gb:BF030448 /FEA=EST /DB_XREF=gi:10738160
235502_at_HG-U133B		ESTs	

			/DB_XREF=est:601558546F1 /CLONE=IMAGE:3828250 /UG=Hs.79204 ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
235521_at_HG-U133B	HOXA3	homeo box A3	Consensus includes gb:AW137982 /FEA=EST /DB_XREF=gi:6142300 /DB_XREF=est:U1-H-B11-ad-b-07-0-UI.s1 /CLONE=IMAGE:2714461 /UG=Hs.222446 ESTs
235604_x_at_HG-U133B		ESTs, Weakly similar to Z208_HUMAN ZINC FINGER PROTEIN 208 [H.sapiens]	Consensus includes gb:A1758697 /FEA=EST /DB_XREF=gi:5152422 /DB_XREF=est:ly23e06.x1 /CLONE=IMAGE:2279938 /UG=Hs.256801 ESTs
235647_at_HG-U133B		ESTs	Consensus includes gb:A1298279 /FEA=EST /DB_XREF=gi:3958015 /DB_XREF=est:qm92a06.x1 /CLONE=IMAGE:1896178 /UG=Hs.293411 ESTs
235674_at_HG-U133B		ESTs	Consensus includes gb:AW575183 /FEA=EST /DB_XREF=gi:7246722 /DB_XREF=est:U1-HF-BKO-aas-f-07-0-UI.s1 /CLONE=IMAGE:3054876 /UG=Hs.13849 ESTs
235692_at_HG-U133B		ESTs	Consensus includes gb:AW024527 /FEA=EST /DB_XREF=gi:5878057 /DB_XREF=est:wy04h07.x1 /CLONE=IMAGE:2528605 /UG=Hs.31922 ESTs
			Consensus includes gb:AW663908 /FEA=EST /DB_XREF=gi:7456447 /DB_XREF=est:hi73d08.x1 /CLONE=IMAGE:2977935 /UG=Hs.241569 ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
235706_at_HG-U133B	CPM	carboxypeptidase M	Consensus includes gb:BE326857 /FEA=EST /DB_XREF=gi:9200633 /DB_XREF=est:hr65h06.x1 /CLONE=IMAGE:3133403 /UG=Hs.99237 ESTs
235719_at_HG-U133B		ESTs	Consensus includes gb:A1057619 /FEA=EST /DB_XREF=gi:3331485 /DB_XREF=est:oy31f09.x1 /CLONE=IMAGE:1667465 /UG=Hs.133423 ESTs, Highly similar to .T42654 hypothetical protein DKFZp434G115.1 H.sapiens
235749_at_HG-U133B			Consensus includes gb:A1492051 /FEA=EST /DB_XREF=gi:4393054 /DB_XREF=est:ig06h08.x1 /CLONE=IMAGE:2108031 /UG=Hs.196169 ESTs
235753_at_HG-U133B		ESTs	Consensus includes gb:A1498747 /FEA=EST /DB_XREF=gi:4390729
235818_at_HG-U133B		ESTs	

			DB_XREF=est:tm64h07.x1 /CLONE=IMAGE:2162941 /UG=Hs.133355 ESTs
235823_at_HG-U133B		Homo sapiens cDNA FLJ32102 fis, clone OCBF2001196	Consensus includes gb:A1763000 /FEA=EST /DB_XREF=gi:5178667 /DB_XREF=est:w05h10.x1 /CLONE=IMAGE:2389411 /UG=Hs.120155 ESTs
235982_at_HG-U133B	FCRH1	Fc receptor-like protein 1	Consensus includes gb:AA677057 /FEA=EST /DB_XREF=gi:2657579 /DB_XREF=est:zj59f11.s1 /CLONE=IMAGE:454605 /UG=Hs.180844 ESTs
236019_at_HG-U133B		ESTs	Consensus includes gb:A1076335 /FEA=EST /DB_XREF=gi:3405513 /DB_XREF=est:oz04a05.x1 /CLONE=IMAGE:1674320 /UG=Hs.19440 ESTs
			Consensus includes gb:BF516337 /FEA=EST /DB_XREF=gi:11601516 /DB_XREF=est:U1-H-BW1-anz-h-12-Q-U1.s1 /CLONE=IMAGE:3084166 /UG=Hs.115772 ESTs, Weakly similar to unknown D.melanogaster
236190_at_HG-U133B		ESTs	Consensus includes gb:AW294080 /FEA=EST /DB_XREF=gi:6700716 /DB_XREF=est:U1-H-B12-ahg-a-04-O-U1.s1 /CLONE=IMAGE:2726670 /UG=Hs.126808 ESTs
236226_at_HG-U133B		ESTs	Consensus includes gb:A1859834 /FEA=EST /DB_XREF=gi:5513439 /DB_XREF=est:wm21a08.x1 /CLONE=IMAGE:2436566 /UG=Hs.155512 ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAMILY SC SEQUENCE
236248_x_at_HG-U133B		ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]	CONTAMINATION WARNING ENTRY H.sapiens
236265_at_HG-U133B		Homo sapiens, clone IMAGE:3887266, mRNA	Consensus includes gb:BF438799 /FEA=EST /DB_XREF=gi:11451316 /DB_XREF=est:nab54b05.x1 /CLONE=IMAGE:3269696 /UG=Hs.88013 ESTs
236280_at_HG-U133B		ESTs	Consensus includes gb:A1225238 /FEA=EST /DB_XREF=gi:3807951 /DB_XREF=est:qx12c04.x1 /CLONE=IMAGE:2001126 /UG=Hs.176920 ESTs
236293_at_HG-U133B		ESTs	Consensus includes gb:BE676335 /FEA=EST /DB_XREF=gi:10036876 /DB_XREF=est:7f27d12.x1 /CLONE=IMAGE:3295895 /UG=Hs.283313 ESTs
236301_at_HG-U133B		Homo sapiens, clone IMAGE:3866403, mRNA	Consensus includes gb:AA789123 /FEA=EST /DB_XREF=gi:2849243 /DB_XREF=est:aa66f03.s1 /CLONE=IMAGE:825917 /UG=Hs.46645 ESTs
236341_at_HG-U133B	CTLA4	cytotoxic T-lymphocyte-associated protein 4	Consensus includes gb:A1733018 /FEA=EST /DB_XREF=gi:5054131 /DB_XREF=est:oh60h01.x5 /CLONE=IMAGE:1471441 /UG=Hs.313929 ESTs
236378_at_HG-U133B		ESTs, Weakly similar to C1B_HUMAN	Consensus includes gb:BF681360 /FEA=EST /DB_XREF=gi:11955255

		SNK INTERACTING PROTEIN 2-28 [H.sapiens]	/DB_XREF=est:602156549F1 /CLONE=IMAGE:4297261 /UG=Hs.231898 ESTs, Weakly similar to A Chain A, Homology-Based Model Of Calcium-Saturated Cib H.sapiens
236458_at_HG-U133B		ESTs	Consensus includes gb:BE875072 /FEA=EST /DB_XREF=gi:10323848 /DB_XREF=est:601485941F1 /CLONE=IMAGE:3888275 /UG=Hs.9002 ESTs
236535_at_HG-U133B	FLJ22116	hypothetical protein FLJ22116 ESTs, Weakly similar to Z295_HUMAN ZINC FINGER PROTEIN 295 [H.sapiens]	Consensus includes gb:AW069285 /FEA=EST /DB_XREF=gi:6024283 /DB_XREF=est:cr43f07.x1 /CLONE=HBMSC_cr43f07 /UG=Hs.159452 ESTs
236557_at_HG-U133B			Consensus includes gb:AW085625 /FEA=EST /DB_XREF=gi:6040777 /DB_XREF=est:xb41d11.x1 /CLONE=IMAGE:2578869 /UG=Hs.186838 ESTs, Weakly similar to Z295_HUMAN ZINC FINGER PROTEIN 295 H.sapiens
236606_at_HG-U133B		ESTs	Consensus includes gb:N50912 /FEA=EST /DB_XREF=gi:1192078 /DB_XREF=est:yy93a05.s1 /CLONE=IMAGE:281072 /UG=Hs.47150 ESTs
236648_at_HG-U133B		ESTs	Consensus includes gb:AI684467 /FEA=EST /DB_XREF=gi:4895761 /DB_XREF=est:wa82d04.x1 /CLONE=IMAGE:2302663 /UG=Hs.144057 ESTs
236656_s_at_HG-U133B		ESTs	Consensus includes gb:AW014647 /FEA=EST /DB_XREF=gi:5863404 /DB_XREF=est:UI-H-BI0p-abd-b-12-Q-UI.s1 /CLONE=IMAGE:2711375 /UG=Hs.265499 ESTs
236707_at_HG-U133B	DAPP1	dual adaptor of phosphotyrosine and 3- phosphoinositides	Consensus includes gb:AA521016 /FEA=EST /DB_XREF=gi:2261559 /DB_XREF=est:aa70f04.s1 /CLONE=IMAGE:826303 /UG=Hs.185375 ESTs
236728_at_HG-U133B		ESTs	Consensus includes gb:AW070437 /FEA=EST /DB_XREF=gi:6025435 /DB_XREF=est:xa11b11.x1 /CLONE=IMAGE:2567997 /UG=Hs.26330 ESTs
236787_at_HG-U133B		ESTs	Consensus includes gb:AW591809 /FEA=EST /DB_XREF=gi:7278974 /DB_XREF=est:xx85d08.x1 /CLONE=IMAGE:2850447 /UG=Hs.126630 ESTs
236796_at_HG-U133B		ESTs	Consensus includes gb:AI052447 /FEA=EST /DB_XREF=gi:3308438 /DB_XREF=est:oz07g04.x1 /CLONE=IMAGE:1674678 /UG=Hs.118659 ESTs
236837_x_at_HG-U133B		ESTs	Consensus includes gb:BE669806 /FEA=EST /DB_XREF=gi:10030347 /DB_XREF=est:7e25b04.x1 /CLONE=IMAGE:3283471 /UG=Hs.129137 ESTs
236854_at_HG-U133B		ESTs	Consensus includes gb:AA743694 /FEA=EST /DB_XREF=gi:2784510

236892_s_at_HG-U133B	HOXB6	homeo box B6	/DB_XREF=est:ny92d07.s1 /CLONE=IMAGE:1285741 /UG=Hs.48984 ESTs Consensus includes gb:BF590528 /FEA=EST /DB_XREF=gi:11682852 /DB_XREF=est:7h36h10.x1 /CLONE=IMAGE:3318115 /UG=Hs.269918 ESTs Consensus includes gb:BE550429 /FEA=EST /DB_XREF=gi:9792121 /DB_XREF=est:7a25b09.x1 /CLONE=IMAGE:3219737 /UG=Hs.143905 ESTs Consensus includes gb:AW080028 /FEA=EST /DB_XREF=gi:6035180 /DB_XREF=est:x011g09.x1 /CLONE=IMAGE:2606848 /UG=Hs.131601 ESTs Consensus includes gb:AI821801 /FEA=EST /DB_XREF=gi:5440880 /DB_XREF=est:nr06c07.x5 /CLONE=IMAGE:1161036 /UG=Hs.168974 ESTs, Highly similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens -
236979_at_HG-U133B		ESTs	Consensus includes gb:AA703523 /FEA=EST /DB_XREF=gi:2713441 /DB_XREF=est:zj12h12.s1 /CLONE=IMAGE:450119 /UG=Hs.24128 ESTs
237006_at_HG-U133B		ESTs	Consensus includes gb:AI871655 /FEA=EST /DB_XREF=gi:5545704 /DB_XREF=est:we28g08.x1 /CLONE=IMAGE:2342462 /UG=Hs.200815 ESTs
237068_at_HG-U133B		ESTs	Consensus includes gb:AI695007 /FEA=EST /DB_XREF=gi:4982907 /DB_XREF=est:we45c09.x1 /CLONE=IMAGE:2344048 /UG=Hs.159362 ESTs
237291_at_HG-U133B		ESTs	Consensus includes gb:AI539318 /FEA=EST /DB_XREF=gi:4453453 /DB_XREF=est:le45f03.x1 /CLONE=IMAGE:2089661 /UG=Hs.115580 ESTs
237337_at_HG-U133B		ESTs	Consensus includes gb:N71063 /FEA=EST /DB_XREF=gi:1227643 /DB_XREF=est:za86a11.s1 /CLONE=IMAGE:299420 /UG=Hs.38173 ESTs
237411_at_HG-U133B	LOC153516	hypothetical protein BC010563	Consensus includes gb:AVW449838 /FEA=EST /DB_XREF=gi:6990614 /DB_XREF=est:UJ-H-BI3-akm-d-12-O-U1.s1 /CLONE=IMAGE:2734894 /UG=Hs.97562 ESTs
237431_at_HG-U133B		ESTs	Consensus includes gb:AI990122 /FEA=EST /DB_XREF=gi:5837003 /DB_XREF=est:ws29d06.x1 /CLONE=IMAGE:2498603 /UG=Hs.196988 ESTs
237864_at_HG-U133B		ESTs	Consensus includes gb:AI620209 /FEA=EST /DB_XREF=gi:4629335 /DB_XREF=est:tu54d10.x1 /CLONE=IMAGE:2254867 /UG=Hs.37916 ESTs
238012_at_HG-U133B		ESTs	

238022_at_HG-U133B		ESTs	Consensus includes gb:AA954994 /FEA=EST /DB_XREF=gi:3118689 /DB_XREF=est:op24f03.s1 /CLONE=IMAGE:1577789 /UG=Hs.237396 ESTs
238026_at_HG-U133B	RPL35A	ribosomal protein L35a	Consensus includes gb:A1458020 /FEA=EST /DB_XREF=gi:4312038 /DB_XREF=est:ij66e05.x1 /CLONE=IMAGE:2146496 /UG=Hs.293287 ESTs
238039_at_HG-U133B		ESTs, Moderately similar to A53959 thromboxane A-2 receptor, endothelial [H.sapiens]	Consensus includes gb:BG180437 /FEA=EST /DB_XREF=gi:12687140 /DB_XREF=est:602331329F1 /CLONE=IMAGE:4432615 /UG=Hs.27167 ESTs
238055_at_HG-U133B			Consensus includes gb:BG505277 /FEA=EST /DB_XREF=gi:13466794 /DB_XREF=est:602551757F1 /CLONE=IMAGE:4663982 /UG=Hs.100501 ESTs, Highly similar to AT1C_HUMAN POTENTIAL PHOSPHOLIPID-TRANSPORTING ATPASE IC H.sapiens
238057_at_HG-U133B		Homo sapiens mRNA; cDNA DKFZp451H032 (from clone DKFZp451H032)	Consensus includes gb:AW195800 /FEA=EST /DB_XREF=gi:6475020 /DB_XREF=est:xn41b09.x1 /CLONE=IMAGE:2696249 /UG=Hs.149401 ESTs
238066_at_HG-U133B	RBP7	retinoid binding protein 7	Consensus includes gb:A1733027 /FEA=EST /DB_XREF=gi:5054140 /DB_XREF=est:oj14a06.x5 /CLONE=IMAGE:1492114 /UG=Hs.292718 ESTs, Weakly similar to RET2_HUMAN RETINOL-BINDING PROTEIN II, CELLULAR H.sapiens
238155_at_HG-U133B		ESTs	Consensus includes gb:A1638235 /FEA=EST /DB_XREF=gi:4690469 /DB_XREF=est:tt12a04.x1 /CLONE=IMAGE:2240526 /UG=Hs.171689 ESTs
238208_at_HG-U133B		ESTs	Consensus includes gb:N53978 /FEA=EST /DB_XREF=gi:1195144 /DB_XREF=est:yv60h12.s1 /CLONE=IMAGE:247175 /UG=Hs.113106 ESTs
238304_at_HG-U133B		ESTs	Consensus includes gb:R45137 /FEA=EST /DB_XREF=gi:823491 /DB_XREF=est:yv39f12.s1 /CLONE=IMAGE:34825 /UG=Hs.21868 ESTs
238365_s_at_HG-U133B		ESTs, Weakly similar to CA13 MOUSE COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [M.musculus]	Consensus includes gb:A1638342 /FEA=EST /DB_XREF=gi:4690576 /DB_XREF=est:tt09g10.x1 /CLONE=IMAGE:2240322 /UG=Hs.158272 ESTs
238367_s_at_HG-		ESTs, Weakly similar to CA13 MOUSE	Consensus includes gb:AW015512 /FEA=EST /DB_XREF=gi:5864269

U133B		COLLAGEN ALPHA 1(III) CHAIN PRECURSOR [M.musculus]	/DB_XREF=est:UH-B10p-aa-u-12-0-UI.s1 /CLONE=IMAGE:2710558 /UG=Hs.158272 ESTs
238376_at_HG-U133B		Homo sapiens cDNA FLJ30967 fis, clone HEART2000309, weakly similar to PTB- ASSOCIATED SPLICING FACTOR	Consensus includes gb:A1436581 /FEA=EST /DB_XREF=gi:4282842 /DB_XREF=est:t03d04.x1 /CLONE=IMAGE:2129383 /UG=Hs.169738 ESTs
238392_at_HG-U133B		ESTs	Consensus includes gb:AW301504 /FEA=EST /DB_XREF=gi:6711181 /DB_XREF=est:xs78a03.x1 /CLONE=IMAGE:2775724 /UG=Hs.145480 ESTs
238516_at_HG-U133B	BMPR2	bone morphogenetic protein receptor, type II (serine/threonine kinase)	Consensus includes gb:BF247383 /FEA=EST /DB_XREF=gi:11162750 /DB_XREF=est:601858146F1 /CLONE=IMAGE:4068634 /UG=Hs.126351 ESTs
238583_at_HG-U133B		ESTs, Weakly similar to YCD1_HUMAN HYPOTHETICAL PROTEIN CGI-131 [H.sapiens]	Consensus includes gb:BG023974 /FEA=EST /DB_XREF=gi:12409070 /DB_XREF=est:602303676F1 /CLONE=IMAGE:4394946 /UG=Hs.133878 ESTs, Weakly similar to AF151889 1 CGI-131 protein H.sapiens
238587_at_HG-U133B	MGC15437	nm23-phosphorylated unknown substrate	Consensus includes gb:A1927919 /FEA=EST /DB_XREF=gi:5663883 /DB_XREF=est:wp03d11.x1 /CLONE=IMAGE:2463765 /UG=Hs.187625 ESTs
238593_at_HG-U133B		ESTs	Consensus includes gb:AW962511 /FEA=EST /DB_XREF=gi:8152347 /DB_XREF=est:EST374584 /UG=Hs.152003 ESTs
238604_at_HG-U133B		ESTs	Consensus includes gb:AA768884 /FEA=EST /DB_XREF=gi:2820122 /DB_XREF=est:nz82e07.s1 /CLONE=IMAGE:1301988 /UG=Hs.140489 ESTs
238651_at_HG-U133B		ESTs	Consensus includes gb:BF512491 /FEA=EST /DB_XREF=gi:11597593 /DB_XREF=est:UH-B13-alw-h-01-0-UI.s1 /CLONE=IMAGE:3069144 /UG=Hs.23096 ESTs
238652_at_HG-U133B		ESTs	Consensus includes gb:AW419203 /FEA=EST /DB_XREF=gi:6947135 /DB_XREF=est:xu31b03.x1 /CLONE=IMAGE:2801741 /UG=Hs.313541 ESTs
238686_at_HG-U133B	FBXO3	F-box only protein 3	Consensus includes gb:AA130258 /FEA=EST /DB_XREF=gi:1691420 /DB_XREF=est:z129c04.r1 /CLONE=IMAGE:503334 /UG=Hs.332421 ESTs
238750_at_HG-U133B		ESTs	Consensus includes gb:AW083576 /FEA=EST /DB_XREF=gi:6038728 /DB_XREF=est:xc18g08.x1 /CLONE=IMAGE:2584670 /UG=Hs.218707 ESTs
238752_at_HG-U133B		ESTs	Consensus includes gb:AA780295 /FEA=EST /DB_XREF=gi:2839626

			/DB_XREF=est:af55h01.s1 /CLONE=IMAGE:1035601 /UG=Hs.122155 ESTs
238756_at_HG-U133B		ESTs	Consensus includes gb:A1860012 /FEA=EST /DB_XREF=gi:5513628 /DB_XREF=est:wm22g09.x1 /CLONE=IMAGE:2436736 /UG=Hs.41294 ESTs
		ESTs, Weakly similar to lectin-like NK cell receptor [Homo sapiens] [H.sapiens]	Consensus includes gb:BE738988 /FEA=EST /DB_XREF=gi:10152980 /DB_XREF=est:601556050F1 /CLONE=IMAGE:3825757 /UG=Hs.156100 ESTs, Weakly similar to c-type lectin DCL1 M.musculus
238790_at_HG-U133B		ESTs, Weakly similar to hypothetical protein FLJ20378 [Homo sapiens] [H.sapiens]	Consensus includes gb:AA282536 /FEA=EST /DB_XREF=gi:1925451 /DB_XREF=est:zs90d12.s1 /CLONE=IMAGE:704759 /UG=Hs.267124 ESTs, Weakly similar to ALU6_HUMAN ALU SUBFAMILY SP SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
238791_at_HG-U133B		Homo sapiens cDNA FLJ30581 fis, clone BRAWH2007069	Consensus includes gb:BF844863 /FEA=EST /DB_XREF=gi:12200793 /DB_XREF=est:MR1-HT1136-221200-009-g07 /UG=Hs.145569 ESTs
238824_at_HG-U133B		Homo sapiens, clone MGC:17708 IMAGE:3868595, mRNA, complete cds	Consensus includes gb:BG108346 /FEA=EST /DB_XREF=gi:12602192 /DB_XREF=est:602280355F1 /CLONE=IMAGE:4368180 /UG=Hs.72045 ESTs
239054_at_HG-U133B		ESTs, Weakly similar to 810024G URF 2 [H.sapiens]	Consensus includes gb:BE348277 /FEA=EST /DB_XREF=gi:9260130 /DB_XREF=est:hw21g08.x1 /CLONE=IMAGE:3183614 /UG=Hs.144616 ESTs, Weakly similar to NADH dehydrogenase subunit 2 H.sapiens
239071_at_HG-U133B		ESTs	Consensus includes gb:A1972451 /FEA=EST /DB_XREF=gi:5769367 /DB_XREF=est:wr39h05.x1 /CLONE=IMAGE:2490105 /UG=Hs.173904 ESTs
239122_at_HG-U133B	IL24	interleukin 24	Consensus includes gb:A1638155 /FEA=EST /DB_XREF=gi:4690389 /DB_XREF=est:ts97a11.x1 /CLONE=IMAGE:2239196 /UG=Hs.176430 ESTs
239152_at_HG-U133B		ESTs	Consensus includes gb:AW263526 /FEA=EST /DB_XREF=gi:6640342 /DB_XREF=est:xn80d07.x1 /CLONE=IMAGE:2700781 /UG=Hs.243023 ESTs
239214_at_HG-U133B		ESTs	Consensus includes gb:AA806831 /FEA=EST /DB_XREF=gi:2876407 /DB_XREF=est:oc29b08.s1 /CLONE=IMAGE:1351095 /UG=Hs.123244 ESTs
239229_at_HG-U133B		ESTs	Consensus includes gb:A1342246 /FEA=EST /DB_XREF=gi:4079173 /DB_XREF=est:qt26g09.x1 /CLONE=IMAGE:1949152 /UG=Hs.50125 ESTs
239231_at_HG-U133B		ESTs, Weakly similar to ALUC_HUMAN	Consensus includes gb:BE464819 /FEA=EST /DB_XREF=gi:9510513



		IIII ALU CLASS C WARNING ENTRY III [H.sapiens]	/DB_XREF=est:hs87d03.x1 /CLONE=IMAGE:3144197 /UG=Hs.63187 ESTs, Weakly similar to ALUC_HUMAN IIII ALU CLASS C WARNING ENTRY III H.sapiens
239263_at_HG-U133B		ESTs	Consensus includes gb:BE905194 /FEA=EST /DB_XREF=gi:10398233 /DB_XREF=est:601499220F1 /CLONE=IMAGE:3901109 /UG=Hs.97855 ESTs
239278_at_HG-U133B		ESTs, Weakly similar to JC5238 galactosylceramide-like protein, GCP [H.sapiens]	Consensus includes gb:A1471969 /FEA=EST /DB_XREF=gi:4334059 /DB_XREF=est:ij85a12.x1 /CLONE=IMAGE:2148286 /UG=Hs.182606 ESTs
239279_at_HG-U133B		ESTs	Consensus includes gb:A1862518 /FEA=EST /DB_XREF=gi:5526625 /DB_XREF=est:wj15a03.x1 /CLONE=IMAGE:2402860 /UG=Hs.158094 ESTs
239287_at_HG-U133B		ESTs	Consensus includes gb:AA769410 /FEA=EST /DB_XREF=gi:2820648 /DB_XREF=est:nz38f06.s1 /CLONE=IMAGE:1290083 /UG=Hs.128654 ESTs
239292_at_HG-U133B		ESTs	Consensus includes gb:AA825563 /FEA=EST /DB_XREF=gi:2898875 /DB_XREF=est:od55c12.s1 /CLONE=IMAGE:1371862 /UG=Hs.124786 ESTs
239302_s_at_HG-U133B		ESTs, Moderately similar to I60307 beta- galactosidase, alpha peptide - Escherichia coli [E.coli]	Consensus includes gb:AA931539 /FEA=EST /DB_XREF=gi:3085925 /DB_XREF=est:oo56a09.s1 /CLONE=IMAGE:1570168 /UG=Hs.293056 ESTs
239393_at_HG-U133B		ESTs	Consensus includes gb:AW510927 /FEA=EST /DB_XREF=gi:7149005 /DB_XREF=est:hd41d06.x1 /CLONE=IMAGE:2912075 /UG=Hs.125243 ESTs
239442_at_HG-U133B		ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]	Consensus includes gb:BF589179 /FEA=EST /DB_XREF=gi:11681503 /DB_XREF=est:nab28d04.x1 /CLONE=IMAGE:3267126 /UG=Hs.173776 ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
239478_x_at_HG-U133B		ESTs	Consensus includes gb:A1761411 /FEA=EST /DB_XREF=gi:5177078 /DB_XREF=est:wg65c03.x1 /CLONE=IMAGE:2369956 /UG=Hs.169812 ESTs
239538_at_HG-U133B		ESTs	Consensus includes gb:BG548811 /FEA=EST /DB_XREF=gi:13547489 /DB_XREF=est:602576251F1 /CLONE=IMAGE:4704372 /UG=Hs.146509 ESTs
239597_at_HG-U133B		ESTs	Consensus includes gb:AA993566 /FEA=EST /DB_XREF=gi:3180111

			ESTs, Weakly similar to chondroitin 4-sulfotransferase [Homo sapiens] [H.sapiens]	/DB_XREF=est:oi96g10.s1 /CLONE=IMAGE:1624674 /UG=Hs.159983 ESTs
239647_at_HG-U133B				Consensus includes gb:AA677272 /FEA=EST /DB_XREF=gi:2657794 /DB_XREF=est:zf61c03.s1 /CLONE=IMAGE:454756 /UG=Hs.117048 ESTs
239651_at_HG-U133B			ESTs	Consensus includes gb:BE671583 /FEA=EST /DB_XREF=gi:10032124 /DB_XREF=est:7e54c10.x1 /CLONE=IMAGE:3286290 /UG=Hs.189394 ESTs
239679_at_HG-U133B			ESTs	Consensus includes gb:AI871160 /FEA=EST /DB_XREF=gi:5545128 /DB_XREF=est:w179g10.x1 /CLONE=IMAGE:2431170 /UG=Hs.163778 ESTs
239699_s_at_HG-U133B			ESTs	Consensus includes gb:AW195920 /FEA=EST /DB_XREF=gi:6475150 /DB_XREF=est:xn86g08.x1 /CLONE=IMAGE:2701406 /UG=Hs.144252 ESTs
239791_at_HG-U133B	HOXB6		homeo box B6	Consensus includes gb:AI125255 /FEA=EST /DB_XREF=gi:3593769 /DB_XREF=est:qd87h09.x1 /CLONE=IMAGE:1736513 /UG=Hs.269918 ESTs
239824_s_at_HG-U133B	MGC10744		hypothetical protein MGC10744	Consensus includes gb:BF971873 /FEA=EST /DB_XREF=gi:12339088 /DB_XREF=est:602240462F1 /CLONE=IMAGE:4328990 /UG=Hs.25092 ESTs
239835_at_HG-U133B	KIAA1842		KIAA1842 protein	Consensus includes gb:AA669114 /FEA=EST /DB_XREF=gi:2630613 /DB_XREF=est:aa81h02.s1 /CLONE=IMAGE:827379 /UG=Hs.116665 ESTs
239956_at_HG-U133B			ESTs	Consensus includes gb:AW291535 /FEA=EST /DB_XREF=gi:6698171 /DB_XREF=est:UI-H-BI2-agk-b-12-O-UI.s1 /CLONE=IMAGE:2724454 /UG=Hs.254980 ESTs
240061_at_HG-U133B			ESTs	Consensus includes gb:AW684903 /FEA=EST /DB_XREF=gi:7457447 /DB_XREF=est:hi85e04.x1 /CLONE=IMAGE:2979102 /UG=Hs.186649 ESTs
240106_at_HG-U133B			ESTs, Weakly similar to A49175 Motch B protein - mouse [M.musculus]	Consensus includes gb:AI633523 /FEA=EST /DB_XREF=gi:4684853 /DB_XREF=est:th68b11.x1 /CLONE=IMAGE:2123805 /UG=Hs.44705 ESTs
240113_at_HG-U133B			ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]	Consensus includes gb:AI732466 /FEA=EST /DB_XREF=gi:5053579 /DB_XREF=est:zn87g06.x5 /CLONE=IMAGE:565210 /UG=Hs.193133 ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
240201_at_HG-U133B			ESTs	Consensus includes gb:AI821995 /FEA=EST /DB_XREF=gi:5441074

			/DB_XREF=est:ok97f07.x5 /CLONE=IMAGE:1521925 /UG=Hs.130173 ESTs
240239_at_HG-U133B	FLJ14779	hypothetical protein FLJ14779	Consensus includes gb:N63953 /FEA=EST /DB_XREF=gi:1211782 /DB_XREF=est:yz81b03.s1 /CLONE=IMAGE:289421 /UG=Hs.243662 ESTs
240269_at_HG-U133B		ESTs	Consensus includes gb:BF590274 /FEA=EST /DB_XREF=gi:11682598 /DB_XREF=est:nab22d01.x1 /CLONE=IMAGE:3266712 /UG=Hs.164923 ESTs
			Consensus includes gb:AW204518 /FEA=EST /DB_XREF=gi:6503990 /DB_XREF=est:U1-H-B11-aei-g-02-Q-U1.s1 /CLONE=IMAGE:2719658 /UG=Hs.244601 ESTs
240449_at_HG-U133B	ZNF341	zinc finger protein 341	Consensus includes gb:BF436632 /FEA=EST /DB_XREF=gi:11449031 /DB_XREF=est:7p09b02.x1 /CLONE=IMAGE:3645243 /UG=Hs.156100 ESTs, Weakly similar to c-type lectin DCL1 M.musculus
240572_s_at_HG-U133B		ESTs, Weakly similar to lectin-like NK cell receptor [Homo sapiens]	Consensus includes gb:AW007727 /FEA=EST /DB_XREF=gi:5856505 /DB_XREF=est:wt68d07.x1 /CLONE=IMAGE:2512621 /UG=Hs.132650 ESTs
240581_at_HG-U133B		ESTs	Consensus includes gb:AW182300 /FEA=EST /DB_XREF=gi:6450760 /DB_XREF=est:xj41a03.x1 /CLONE=IMAGE:2659756 /UG=Hs.112612 ESTs
240740_at_HG-U133B		ESTs	Consensus includes gb:BE671136 /FEA=EST /DB_XREF=gi:10031677 /DB_XREF=est:7e46d12.x1 /CLONE=IMAGE:3285527 /UG=Hs.243602 ESTs
240785_at_HG-U133B		ESTs	Consensus includes gb:N56968 /FEA=EST /DB_XREF=gi:1200858 /DB_XREF=est:yy56b01.s1 /CLONE=IMAGE:277513 /UG=Hs.46707
240801_at_HG-U133B	C21orf37	chromosome 21 open reading frame 37	Consensus includes gb:AA853996 /FEA=EST /DB_XREF=gi:2941534 /DB_XREF=est:aj52a02.s1 /CLONE=IMAGE:1393898 /UG=Hs.269757 ESTs, Weakly similar to B34087 hypothetical protein H.sapiens
240842_at_HG-U133B		ESTs	Consensus includes gb:AW471181 /FEA=EST /DB_XREF=gi:7041287 /DB_XREF=est:xv13b04.x1 /CLONE=IMAGE:2812975 /UG=Hs.160874 ESTs
241353_s_at_HG-U133B		ESTs	Consensus includes gb:AA278233 /FEA=EST /DB_XREF=gi:1920173 /DB_XREF=est:zs77a10.r1 /CLONE=IMAGE:703482 /UG=Hs.100591 ESTs
241370_at_HG-U133B		ESTs	Consensus includes gb:H05959 /FEA=EST /DB_XREF=gi:869511
241383_at_HG-U133B		ESTs	

			/DB_XREF=est:i76d05.s1 /CLONE=IMAGE:44004 /UG=Hs.62189 ESTs
			Consensus includes gb:AL572553 /FEA=EST /DB_XREF=gi:12930334
			/DB_XREF=est:AL572553 /CLONE=CS0D1008YD03 (3 prime) /UG=Hs.145990
241395_at_HG-U133B		ESTs	ESTs
			Consensus includes gb:N92599 /FEA=EST /DB_XREF=gi:1264908
241421_at_HG-U133B		ESTs	/DB_XREF=est:zb27d04.s1 /CLONE=IMAGE:304807 /UG=Hs.130694 ESTs
241464_s_at_HG-U133B		ESTs	Consensus includes gb:AI973033 /FEA=EST /DB_XREF=gi:5769859
			/DB_XREF=est:wr46g03.x1 /CLONE=IMAGE:2490772 /UG=Hs.126691 ESTs
241483_at_HG-U133B		ESTs	Consensus includes gb:AA156795 /FEA=EST /DB_XREF=gi:1728410
			/DB_XREF=est:z120a03.s1 /CLONE=IMAGE:502444 /UG=Hs.62772 ESTs
241525_at_HG-U133B		ESTs	Consensus includes gb:AV700191 /FEA=EST /DB_XREF=gi:10302162
			/DB_XREF=est:AV700191 /CLONE=GKCEKG11 /UG=Hs.132051 ESTs
241734_at_HG-U133B		Homo sapiens cDNA FLJ25286 fis, clone STM06909	Consensus includes gb:AI391443 /FEA=EST /DB_XREF=gi:4217447
			/DB_XREF=est:tf9e06.x1 /CLONE=IMAGE:2107138 /UG=Hs.107622 ESTs
241742_at_HG-U133B	PRAM-1	PRAM-1 protein	Consensus includes gb:AW027174 /FEA=EST /DB_XREF=gi:5885930
			/DB_XREF=est:wt72c10.x1 /CLONE=IMAGE:2513010 /UG=Hs.239276 ESTs, Weakly similar to FYB_HUMAN FYN-BINDING PROTEIN H.sapiens
241754_at_HG-U133B		ESTs	Consensus includes gb:AA829836 /FEA=EST /DB_XREF=gi:2902935
			/DB_XREF=est:od40c07.s1 /CLONE=IMAGE:1370412 /UG=Hs.59504 ESTs
241795_at_HG-U133B		ESTs	Consensus includes gb:AA678073 /FEA=EST /DB_XREF=gi:2658595
			/DB_XREF=est:z12g12.s1 /CLONE=IMAGE:430630 /UG=Hs.129827 ESTs
			Consensus includes gb:BF509144 /FEA=EST /DB_XREF=gi:11592442
			/DB_XREF=est:UI-H-B14-aov-a-05-O-UI.s1 /CLONE=IMAGE:3086097
241810_at_HG-U133B		ESTs	/UG=Hs.202088 ESTs
241930_x_at_HG-U133B		ESTs	Consensus includes gb:AA223204 /FEA=EST /DB_XREF=gi:1843755
			/DB_XREF=est:zt06c05.s1 /CLONE=IMAGE:650696 /UG=Hs.186898 ESTs
241969_at_HG-U133B	ITM2B	Integral membrane protein 2B	Consensus includes gb:AA150242 /FEA=EST /DB_XREF=gi:1721773
			/DB_XREF=est:z107c04.s1 /CLONE=IMAGE:491622 /UG=Hs.323529 ESTs,

			Highly similar to S27963 modulator recognition factor 2 H.sapiens
241975_at_HG-U133B		ESTs	Consensus includes gb:N29850 /FEA=EST /DB_XREF=gi:1148370 /DB_XREF=est:yw94a12.s1 /CLONE=IMAGE:259870 /UG=Hs.44098 ESTs
241985_at_HG-U133B		ESTs	Consensus includes gb:A1814405 /FEA=EST /DB_XREF=gi:5425620 /DB_XREF=est:wj72g03.x1 /CLONE=IMAGE:2408404 /UG=Hs.224569 ESTs
242065_x_at_HG-U133B	KIAA0982	KIAA0982 protein	Consensus includes gb:BG477984 /FEA=EST /DB_XREF=gi:13410263 /DB_XREF=est:602522982F1 /CLONE=IMAGE:4641356 /UG=Hs.147801 ESTs
242104_at_HG-U133B		ESTs, Moderately similar to PRO0478 protein [Homo sapiens] [H.sapiens]	Consensus includes gb:AA826288 /FEA=EST /DB_XREF=gi:2899600 /DB_XREF=est:od03h09.s1 /CLONE=IMAGE:1358177 /UG=Hs.191782 ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
242223_at_HG-U133B		ESTs	Consensus includes gb:AA505323 /FEA=EST /DB_XREF=gi:2241460 /DB_XREF=est:nh83c08.s1 /CLONE=IMAGE:965102 /UG=Hs.151609 ESTs
242292_at_HG-U133B		Homo sapiens, similar to melanoma antigen, family A, 11, clone MGC:34827 IMAGE:5199470, mRNA, complete cds	Consensus includes gb:H12084 /FEA=EST /DB_XREF=gi:876904 Weakly similar to MAGE-B4 H.sapiens
242329_at_HG-U133B		ESTs	Consensus includes gb:AW071804 /FEA=EST /DB_XREF=gi:6026729 /DB_XREF=est:ws53h03.x1 /CLONE=IMAGE:2500949 /UG=Hs.152541 ESTs
242363_at_HG-U133B		ESTs	Consensus includes gb:BF592008 /FEA=EST /DB_XREF=gi:11684332 /DB_XREF=est:7o35e09.x1 /CLONE=IMAGE:3576280 /UG=Hs.87372 ESTs
242388_x_at_HG-U133B		ESTs	Consensus includes gb:AW576600 /FEA=EST /DB_XREF=gi:7248139 /DB_XREF=est:UJ-HF-BR0p-ajy-c-07-0-U1.s1 /CLONE=IMAGE:3076212 /UG=Hs.123581 ESTs
242404_at_HG-U133B		ESTs	Consensus includes gb:AW518888 /FEA=EST /DB_XREF=gi:7156970 /DB_XREF=est:ha45g06.x1 /CLONE=IMAGE:2876698 /UG=Hs.40937 ESTs
242414_at_HG-U133B		ESTs	Consensus includes gb:AW960707 /FEA=EST /DB_XREF=gi:8150391 /DB_XREF=est:EST372778 /UG=Hs.148324 ESTs
242434_at_HG-U133B		Homo sapiens cDNA FLJ131093 fis, clone	Consensus includes gb:AW771952 /FEA=EST /DB_XREF=gi:7704001

	IMR321000161	/DB_XREF=est:hm66h01.x1 /CLONE=IMAGE:3032881 /UG=Hs.191581 ESTs
		Consensus includes gb:A1800895 /FEA=EST /DB_XREF=gi:5366367
		/DB_XREF=est:wg14b02.x1 /CLONE=IMAGE:2365035 /UG=Hs.131929 ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
242448_at_HG-U133B		Consensus includes gb:AA721230 /FEA=EST /DB_XREF=gi:2737365
242458_at_HG-U133B		/DB_XREF=est:nz72b04.s1 /CLONE=IMAGE:1300975 /UG=Hs.102398 ESTs
		Consensus includes gb:A1620827 /FEA=EST /DB_XREF=gi:4629953
242463_x_at_HG-U133B		/DB_XREF=est:tu86c12.x1 /CLONE=IMAGE:2257942 /UG=Hs.116391 ESTs, Weakly similar to A32891 finger protein 1, placental H.sapiens
242520_s_at_HG-U133B		Consensus includes gb:AW511110 /FEA=EST /DB_XREF=gi:7149188
		/DB_XREF=est:hd43d06.x1 /CLONE=IMAGE:2912267 /UG=Hs.193754 ESTs
		Consensus includes gb:AA747436 /FEA=EST /DB_XREF=gi:2787394
242525_at_HG-U133B		/DB_XREF=est:nx88f10.s1 /CLONE=IMAGE:1269355 /UG=Hs.163105 ESTs
		Consensus includes gb:AV692159 /FEA=EST /DB_XREF=gi:10294022
242541_at_HG-U133B	ABCA9	/DB_XREF=est:AV692159 /CLONE=GKCAOB12 /UG=Hs.301496 ESTs
		Consensus includes gb:AA829635 /FEA=EST /DB_XREF=gi:2902734
242633_x_at_HG-U133B		/DB_XREF=est:od35a09.s1 /CLONE=IMAGE:1369912 /UG=Hs.186589 ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY H.sapiens
		Consensus includes gb:BF512254 /FEA=EST /DB_XREF=gi:11597433
		/DB_XREF=est:UI-H-BW1-amb-a-09-O-UI.s1 /CLONE=IMAGE:3069209 /UG=Hs.126767 ESTs
242695_at_HG-U133B		Consensus includes gb:BE551384 /FEA=EST /DB_XREF=gi:9793076
		/DB_XREF=est:7b64a09.x1 /CLONE=IMAGE:3232984 /UG=Hs.166999 ESTs, Moderately similar to I38344 titin, cardiac muscle H.sapiens
242729_at_HG-U133B		Consensus includes gb:BG402859 /FEA=EST /DB_XREF=gi:13296307
242738_s_at_HG-U133B		/DB_XREF=est:602418552F1 /CLONE=IMAGE:4525500 /UG=Hs.163208 ESTs

242774_at_HG-U133B	SYNE-2	synaptic nuclei expressed gene 2	Consensus includes gb:AI694761 /FEA=EST /DB_XREF=gi:4896055 /DB_XREF=est:wa85h04.x1 /CLONE=IMAGE:2302999 /UG=Hs.201552 ESTs, Weakly similar to T17288 hypothetical protein DKFZp434P1550.1 H.sapiens
242845_at_HG-U133B			Consensus includes gb:AI366780 /FEA=EST /DB_XREF=gi:4136525 /DB_XREF=est:qq41d08.x1 /CLONE=IMAGE:1935087 /UG=Hs.144995 ESTs
242866_x_at_HG-U133B		ESTs	Consensus includes gb:BF509229 /FEA=EST /DB_XREF=gi:11592527 /DB_XREF=est:UI-H-BI4-aow-a-04-O-UI.s1 /CLONE=IMAGE:3086118 /UG=Hs.147381 ESTs
242932_at_HG-U133B		ESTs	Consensus includes gb:AW292329 /FEA=EST /DB_XREF=gi:6698965 /DB_XREF=est:UI-H-BI2-agy-h-05-O-UI.s1 /CLONE=IMAGE:2726240 /UG=Hs.163481 ESTs
242975_s_at_HG-U133B	GNAS	GNAS complex locus	Consensus includes gb:AV753357 /FEA=EST /DB_XREF=gi:10911205 /DB_XREF=est:AV753357 /CLONE=NPDAVC03 /UG=Hs.159354 ESTs
243000_at_HG-U133B		Homo sapiens cDNA FLJ1360 fis, clone MESAN2000572	Consensus includes gb:AW194766 /FEA=EST /DB_XREF=gi:6473684 /DB_XREF=est:xn31a04.x1 /CLONE=IMAGE:2695278 /UG=Hs.209382 ESTs
243020_at_HG-U133B		ESTs	Consensus includes gb:R06738 /FEA=EST /DB_XREF=gi:757358 /DB_XREF=est:yf11a03.s1 /CLONE=IMAGE:126508 /UG=Hs.220823 ESTs
243024_at_HG-U133B		ESTs, Weakly similar to I38598 zinc finger protein ZNF132 [H.sapiens]	Consensus includes gb:AI024029 /FEA=EST /DB_XREF=gi:3239073 /DB_XREF=est:ow70f06.s1 /CLONE=IMAGE:1652195 /UG=Hs.293707 ESTs, Weakly similar to I38598 zinc finger protein ZNF132 H.sapiens
243030_at_HG-U133B		ESTs	Consensus includes gb:AA211369 /FEA=EST /DB_XREF=gi:1810023 /DB_XREF=est:zp51h10.s1 /CLONE=IMAGE:613027 /UG=Hs.269493 ESTs
243154_at_HG-U133B		ESTs	Consensus includes gb:AA215381 /FEA=EST /DB_XREF=gi:1815191 /DB_XREF=est:zr97c09.s1 /CLONE=IMAGE:683632 /UG=Hs.86650 ESTs
243228_at_HG-U133B		ESTs	Consensus includes gb:BF980709 /FEA=EST /DB_XREF=gi:12383456 /DB_XREF=est:602303749F1 /CLONE=IMAGE:4395156 /UG=Hs.32406 ESTs
243362_s_at_HG-U133B	LEF1	lymphoid enhancer-binding factor 1	Consensus includes gb:AA992805 /FEA=EST /DB_XREF=gi:3178539 /DB_XREF=est:oi85a07.s1 /CLONE=IMAGE:1623540 /UG=Hs.171865 ESTs

243363_at_HG-U133B	LEF1	lymphoid enhancer-binding factor 1	Consensus includes gb:AA992805 /FEA=EST /DB_XREF=gi:3178539 /DB_XREF=est:oi85a07.s1 /CLONE=IMAGE:1623540 /UG=Hs.171865 ESTs
243493_at_HG-U133B		ESTs	Consensus includes gb:T97977 /FEA=EST /DB_XREF=gi:747322 /DB_XREF=est:ye58g09.s1 /CLONE=IMAGE:121984 /UG=Hs.60260 ESTs
243538_at_HG-U133B		ESTs	Consensus includes gb:AA738314 /FEA=EST /DB_XREF=gi:2769071 /DB_XREF=est:nx16g04.s1 /CLONE=IMAGE:1256310 /UG=Hs.5840 ESTs
			Consensus includes gb:BF029215 /FEA=EST /DB_XREF=gi:10736927 /DB_XREF=est:601765432F1 /CLONE=IMAGE:3997687 /UG=Hs.173179 ESTs, Weakly similar to JW0079 heterogeneous nuclear ribonucleoprotein homolog
243579_at_HG-U133B	MSI2	musashi homolog 2 (Drosophila)	JKTBP H.sapiens Consensus includes gb:A1057226 /FEA=EST /DB_XREF=gi:3331092 /DB_XREF=est:oz11c08.x1 /CLONE=IMAGE:1675022 /UG=Hs.120855 ESTs
243756_at_HG-U133B		ESTs	Consensus includes gb:AW085312 /FEA=EST /DB_XREF=gi:6040464 /DB_XREF=est:xe08f05.x1 /CLONE=IMAGE:2606529 /UG=Hs.177164 ESTs
243764_at_HG-U133B		ESTs	Consensus includes gb:AW575863 /FEA=EST /DB_XREF=gi:7247498 /DB_XREF=est:UI-HF-BLO-aci-e-03-O-UI.s1 /CLONE=IMAGE:3059045 /UG=Hs.136232 ESTs
243780_at_HG-U133B		ESTs	Consensus includes gb:A1436580 /FEA=EST /DB_XREF=gi:4282834 /DB_XREF=est:ti03d03.x1 /CLONE=IMAGE:2129381 /UG=Hs.257490 ESTs
243798_at_HG-U133B		ESTs	Consensus includes gb:AW237390 /FEA=EST /DB_XREF=gi:6569779 /DB_XREF=est:xm71b10.x1 /CLONE=IMAGE:2689627 /UG=Hs.250488 ESTs
243859_at_HG-U133B		ESTs	Consensus includes gb:A1286254 /FEA=EST /DB_XREF=gi:3924487 /DB_XREF=est:qu91a02.x1 /CLONE=IMAGE:1979402 /UG=Hs.149809 ESTs
243932_at_HG-U133B		ESTs	Consensus includes gb:A1572979 /FEA=EST /DB_XREF=gi:4536353 /DB_XREF=est:tn64g01.x1 /CLONE=IMAGE:2174352 /UG=Hs.174767 ESTs
243968_x_at_HG-U133B		ESTs	Consensus includes gb:AA777639 /FEA=EST /DB_XREF=gi:2837118 /DB_XREF=est:zi95c04.s1 /CLONE=IMAGE:448518 /UG=Hs.118088 ESTs
244147_at_HG-U133B		ESTs	Consensus includes gb:AW263527 /FEA=EST /DB_XREF=gi:6640343
244230_at_HG-U133B		ESTs	



			/DB_XREF=est:xn80d08.x1 /CLONE=IMAGE:2700783 /UG=Hs.293142 ESTs
			Consensus includes gb:A1129850 /FEA=EST /DB_XREF=gi:3598364
244248_at_HG-U133B		ESTs	/DB_XREF=est:qc35a12.x1 /CLONE=IMAGE:1711582 /UG=Hs.133396 ESTs
			Consensus includes gb:A1363185 /FEA=EST /DB_XREF=gi:4114806
244257_at_HG-U133B		ESTs	/DB_XREF=est:qy68e05.x1 /CLONE=IMAGE:2017184 /UG=Hs.192121 ESTs
			Consensus includes gb:AW340139 /FEA=EST /DB_XREF=gi:6836765
244261_at_HG-U133B		ESTs	/DB_XREF=est:hc93h01.x1 /CLONE=IMAGE:2907601 /UG=Hs.105866 ESTs
			Consensus includes gb:AW104453 /FEA=EST /DB_XREF=gi:6075188
244523_at_HG-U133B	MMD	monocyte to macrophage differentiation-associated	/DB_XREF=est:xd78b02.x1 /CLONE=IMAGE:2603691 /UG=Hs.99734 ESTs
			Consensus includes gb:AA552017 /FEA=EST /DB_XREF=gi:2322269
244550_at_HG-U133B		ESTs	/DB_XREF=est:ng01g11.s1 /CLONE=IMAGE:928196 /UG=Hs.162245 ESTs
			Consensus includes gb:AL042699 /FEA=EST /DB_XREF=gi:5422148
244636_at_HG-U133B		ESTs	/DB_XREF=est:DKFZp434P0421.s1 /CLONE=DKFZp434P0421 /UG=Hs.209222 ESTs
			Consensus includes gb:AW444868 /FEA=EST /DB_XREF=gi:6988630
244652_at_HG-U133B		ESTs	/DB_XREF=est:UI-H-B13-ajz-a-11-Q-UI.s1 /CLONE=IMAGE:2733237 /UG=Hs.190129 ESTs
			Consensus includes gb:BE85713 /FEA=EST /DB_XREF=gi:10368199
244740_at_HG-U133B		Homo sapiens, clone MGC:9913 IMAGE:3870821, mRNA, complete cds	/DB_XREF=est:7g08d09.x1 /CLONE=IMAGE:3305873 /UG=Hs.23133 ESTs, Weakly similar to A33569 alcohol sulfoltransferase R.norvegicus
			Consensus includes gb:BF112140 /FEA=EST /DB_XREF=gi:10941830
244876_at_HG-U133B		ESTs	/DB_XREF=est:7140g11.x1 /CLONE=IMAGE:3524156 /UG=Hs.191950 ESTs
266_s_at_HG-U133A	CD24	CD24 antigen (small cell lung carcinoma cluster 4 antigen)	L33930 /FEATURE= /DEFINITION=HUMCD24B Homo sapiens CD24 signal transducer mRNA, complete cds and 3' region
		protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma)	Cluster Incl. S46622-calcineurin A catalytic subunit [human, testis, mRNA, 2134 nt] /cds=(286,1794) /gb=S46622 /gi=258000 /ug=Hs.75206 /len=2134
32541_at_HG-U133A	PPP3CC		Cluster Incl. N90866-zb11b10.s1 Homo sapiens cDNA, 3' end /clone=IMAGE-
34210_at_HG-U133A	CDW52	CDW52 antigen (CAMPATH-1 antigen)	

34689_at_HG-U133A	TREX1	three prime repair exonuclease 1	301723 /clone_end=3' /gb=N90866 /gi=1444193 /ug=Hs.214742- /len=577
34726_at_HG-U133A	CACNB3	calcium channel, voltage-dependent, beta 3 subunit	Cluster Incl. AJ243797:Homo sapiens mRNA for deoxyribonuclease III (dm3 gene) /cds=(256,1170) /gb=AJ243797 /gi=5524926 /ug=Hs.23595 /len=1239 Cluster Incl. U07139:Human voltage-gated calcium channel beta subunit mRNA, complete cds /cds=(34,1488) /gb=U07139 /gi=463890 /ug=Hs.239447 /len=2532
35666_at_HG-U133A	SEMA3F	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F	Cluster Incl. U38276:Human semaphorin III family homolog mRNA, complete cds /cds=(315,2576) /gb=U38276 /gi=1061350 /ug=Hs.32981 /len=3534
35974_at_HG-U133A	LRMP	lymphoid-restricted membrane protein	Cluster Incl. U10485:Human lymphoid-restricted membrane protein (Jaw1) mRNA, complete cds /cds=(574,2241) /gb=U10485 /gi=505685 /ug=Hs.40202 /len=2417
36004_at_HG-U133A	IKBK	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma	Cluster Incl. AF074382:Homo sapiens Ikb kinase gamma subunit (IKK-gamma) mRNA, complete cds /cds=(148,1407) /gb=AF074382 /gi=3641279 /ug=Hs.43505 /len=1976
36566_at_HG-U133A	CTNS	cystinosis, nephropathic	Cluster Incl. AJ222967 /gi=3036839 /ug=Hs.64837 /len=2611
36612_at_HG-U133A	KIAA0280	KIAA0280 protein	Cluster Incl. D87470:Human mRNA for KIAA0280 gene, partial cds /cds=(0,876) /gb=D87470 /gi=1665822 /ug=Hs.75400 /len=6837
36920_at_HG-U133A	MTM1	myotubular myopathy 1	Cluster Incl. U46024:Homo sapiens myotubularin (MTM1) mRNA, complete cds /cds=(54,1865) /gb=U46024 /gi=1378039 /ug=Hs.75302 /len=3411
37152_at_HG-U133A	PPARD	peroxisome proliferative activated receptor, delta	Cluster Incl. L07592:Human peroxisome proliferator activated receptor mRNA, complete cds /cds=(337,1662) /gb=L07592 /gi=190229 /ug=Hs.106415 /len=3301
37424_at_HG-U133A	HCR	HCR (a-helix coiled-coil rod homologue)	Cluster Incl. AB029343:Homo sapiens HCR (a-helix coiled-coil rod homologue) gene, complete cds /cds=(22,2292) /gb=AB029343 /gi=5360900 /ug=Hs.110746 /len=2445
37831_at_HG-U133A	KIAA0545	KIAA0545 protein	Cluster Incl. AB01117:Homo sapiens mRNA for KIAA0545 protein, partial

			cds /cds=(0,3390) /gb=AB011117 /gi=3043613 /ug=Hs.129943 /len=5520
38149_at_HG-U133A	KIAA0053	KIAA0053 gene product	Cluster Incl. D29842:Human mRNA for KIAA0053 gene, complete cds /cds=(193,2109) /gb=D29642 /gi=473934 /ug=Hs.1528 /len=2739
38269_at_HG-U133A	PKD2	protein kinase D2	Cluster Incl. AL050147:Homo sapiens mRNA; cDNA DKFZp586E0820 (from clone DKFZp586E0820) /cds=(0,1630) /gb=AL050147 /gi=4884153 /ug=Hs.91146 /len=1837
38340_at_HG-U133A	HIP12	huntingtin interacting protein 12	Cluster Incl. AB014555:Homo sapiens mRNA for KIAA0655 protein, partial cds /cds=(0,3253) /gb=AB014555 /gi=3327123 /ug=Hs.96731 /len=4457
38487_at_HG-U133A	FLJ12442	hypothetical protein FLJ12442	Cluster Incl. D87433:Human mRNA for KIAA0246 gene, partial cds /cds=(0,6639) /gb=D87433 /gi=1665760 /ug=Hs.84753 /len=6777
39650_s_at_HG-U133A	KIAA0435	KIAA0435 gene product	Cluster Incl. AB007895:Homo sapiens KIAA0435 mRNA, complete cds /cds=(1195,3528) /gb=AB007895 /gi=2662150 /ug=Hs.31438 /len=5347
39835_at_HG-U133A	SBF1	SET binding factor 1	Cluster Incl. U93181:Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds /cds=(0,5095) /gb=U93181 /gi=3015537 /ug=Hs.112049 /len=5228
40148_at_HG-U133A	APBB2	amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like)	Cluster Incl. U62325:Human FE65-like protein (hFE65L) mRNA, partial cds /cds=(0,2194) /gb=U62325 /gi=1657751 /ug=Hs.15740 /len=2896
40189_at_HG-U133A	SET	SET translocation (myeloid leukemia-associated)	Cluster Incl. M93651:Human set gene, complete cds /cds=(3,836) /gb=M93651 /gi=338038 /ug=Hs.145279 /len=2562
41220_at_HG-U133A	MSF	MLL septin-like fusion	Cluster Incl. AB023208:Homo sapiens mRNA for KIAA0991 protein, complete cds /cds=(732,2000) /gb=AB023208 /gi=4589625 /ug=Hs.181002 /len=3938
41553_at_HG-U133A	C8orf1	chromosome 8 open reading frame 1	Cluster Incl. AI738702:wi22b11.x1 Homo sapiens cDNA, 3' end /clone=IMAGE-2390973 /clone_end=3' /gb=AI738702 /gi=5100683 /ug=Hs.40539 /len=650
41577_at_HG-U133A	PPP1R16B	protein phosphatase 1, regulatory (inhibitor) subunit 16B	Cluster Incl. AB020630:Homo sapiens mRNA for KIAA0823 protein, partial cds /cds=(0,1239) /gb=AB020630 /gi=4240131 /ug=Hs.45719 /len=5597
41660_at_HG-U133A	CELSR1	cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog,	Cluster Incl. AL031586:dJ1163J1.1 (ortholog of mouse transmembrane receptor Celsr1 (KIAA0279 LIKE EGF-like domain containing protein similar

		Drosophila)	to rat MEG /cds=(0.4433) /gb=AL031588 /gi=4007108 /ug=Hs.123043 /len=6438
44065_at_HG-U133A	FLJ14827	hypothetical protein FLJ14827	Cluster Incl. AI937468:wp77e05.x1 Homo sapiens cDNA, 3' end /clone=IMAGE-2467808 /clone_end=3' /gb=AI937468 /gi=5676338 /ug=Hs.235849 /len=516
44563_at_HG-U133A	FLJ10385	hypothetical protein FLJ10385	Cluster Incl. AI858000:wf69b05.x1 Homo sapiens cDNA, 3' end /clone=IMAGE-2408049 /clone_end=3' /gb=AI858000 /gi=5511616 /ug=Hs.30922 /len=715
44669_at_HG-U133A		ESTs, Weakly similar to SYN1 MOUSE SYNAPSIN I [M.musculus]	Cluster Incl. N31716:yy15c12.s1 Homo sapiens cDNA, 3' end /clone=IMAGE-271318 /clone_end=3' /gb=N31716 /gi=1152115 /ug=Hs.31754 /len=624
44790_s_at_HG-U133A	FLJ21562	hypothetical protein FLJ21562	Cluster Incl. AI429310:qc48a05.x1 Homo sapiens cDNA, 3' end /clone=IMAGE-1712816 /clone_end=3' /gb=AI129310 /gi=3597824 /ug=Hs.234923 /len=811
45633_at_HG-U133A	FLJ13912	hypothetical protein FLJ13912	Cluster Incl. AI421812:ff55a07.x1 Homo sapiens cDNA, 3' end /clone=IMAGE-2103156 /clone_end=3' /gb=AI421812 /gi=4267743 /ug=Hs.47125 /len=556
46142_at_HG-U133A	FLJ12681	hypothetical protein FLJ12681	Cluster Incl. AI003763:ou91e02.x1 Homo sapiens cDNA, 3' end /clone=IMAGE-1635194 /clone_end=3' /gb=AI003763 /gi=3213273 /ug=Hs.58362 /len=594
49306_at_HG-U133A	AD037	AD037 protein	Cluster Incl. AI890191:wm79f05.x1 Homo sapiens cDNA, 3' end /clone=IMAGE-2442177 /clone_end=3' /gb=AI890191 /gi=5595355 /ug=Hs.239937 /len=674
49485_at_HG-U133A	PRDM4	PR domain containing 4	Cluster Incl. W22625:71E5 Homo sapiens cDNA /clone=(not-directional) /gb=W22625 /gi=1299507 /ug=Hs.21807 /len=632
50221_at_HG-U133A		Homo sapiens, Similar to transcription factor EB, clone IMAGE:3944945, mRNA, partial cds	Cluster Incl. AI524138:th09f03.x1 Homo sapiens cDNA, 3' end /clone=IMAGE-2117789 /clone_end=3' /gb=AI524138 /gi=4438273 /ug=Hs.23391 /len=834
50277_at_HG-U133A	GGA1	golgi associated, gamma adaptin ear	Cluster Incl. AM001443:wu31e12.x1 Homo sapiens cDNA, 3' end

		containing, ARF binding protein 1	/clone=IMAGE-990785 /clone_end=3' /gb=AW001443 /gi=5848359 /ug=Hs.239110 /len=490
			Cluster Incl. AA134926:zo23d02.s1 Homo sapiens cDNA, 3' end /clone=IMAGE-587715 /clone_end=3' /gb=AA134926 /gi=1696027 /ug=Hs.29173 /len=535
51192_at_HG-U133A	SSH-3	slingshot 3	Cluster Incl. AA868332:ak40h05.s1 Homo sapiens cDNA, 3' end /clone=IMAGE-1408473 /clone_end=3' /gb=AA868332 /gi=2963777 /ug=Hs.77978 /len=481
54970_at_HG-U133A	DKFZP76112123	KIAA1886 protein	Cluster Incl. AA534198:n21a11.s1 Homo sapiens cDNA, 3' end /clone=IMAGE-993116 /clone_end=3' /gb=AA534198 /gi=2278214 /ug=Hs.86392 /len=603
55093_at_HG-U133A	KIAA1402	KIAA1402 protein	Cluster Incl. AA150165:z106h03.r1 Homo sapiens cDNA, 5' end /clone=IMAGE-491573 /clone_end=5' /gb=AA150165 /gi=1721695 /ug=Hs.20102 /len=576
56256_at_HG-U133A	LOC51092	CGI-40 protein	Cluster Incl. A1806628:wf14g08.x1 Homo sapiens cDNA, 3' end /clone=IMAGE-2350622 /clone_end=3' /gb=A1806628 /gi=5393194 /ug=Hs.109778 /len=557
56919_at_HG-U133A	KIAA1449	WD repeat endosomal protein	
		solute carrier family 24 (sodium/potassium/calcium exchanger), member 3	Cluster Incl. R62432:yg52e11.s1 Homo sapiens cDNA, 3' end /clone=IMAGE- 36023 /clone_end=3' /gb=R62432 /gi=834311 /ug=Hs.12321 /len=487
57588_at_HG-U133A	SLC24A3		Cluster Incl. R42449:yg02a07.s1 Homo sapiens cDNA, 3' end /clone=IMAGE- 30831 /clone_end=3' /gb=R42449 /gi=817213 /ug=Hs.235831 /len=431
58780_s_at_HG-U133A	FLJ10357	hypothetical protein FLJ10357	Cluster Incl. AA582932:mn80a11.s1 Homo sapiens cDNA, 3' end /clone=IMAGE-1090172 /clone_end=3' /gb=AA582932 /gi=2360292 /ug=Hs.21349 /len=614
59697_at_HG-U133A		ESTs, Weakly similar to RAB8_HUMAN RAS-RELATED PROTEIN RAB-8 [H.sapiens]	L42374 /FEATURE=mrna /DEFINITION=HUMPP2ABA Homo sapiens protein phosphatase 2A B56-beta (PP2A) mRNA, complete cds
635_s_at_HG-U133A	PPP2R5B	protein phosphatase 2, regulatory subunit B (B56), beta isoform	Cluster Incl. A1937160:wp73h02.x1 Homo sapiens cDNA, 3' end
64942_at_HG-U133A		ESTs	

			/clone=IMAGE-2467443 /clone_end=3' /gb=AI937160 /gi=5676030 /ug=Hs.7967 /len=552
74694_s_at_HG-U133A	FLJ23282	hypothetical protein FLJ23282	Cluster Incl. AA907940:oi24e02.s1 Homo sapiens cDNA, 3' end /clone=IMAGE-1524410 /clone_end=3' /gb=AA907940 /gi=3041944 /ug=Hs.234006 /len=404
77508_r_at_HG-U133A	FLJ23282	hypothetical protein FLJ23282	Cluster Incl. AW001436:wu31e04.x1 Homo sapiens cDNA, 3' end /clone=IMAGE-990769 /clone_end=3' /gb=AW001436 /gi=5848352 /ug=Hs.170253 /len=471
90610_at_HG-U133A	LRRN1	leucine-rich repeat protein, neuronal 1	Cluster Incl. AI654857:wb65b10.x1 Homo sapiens cDNA, 3' end /clone=IMAGE-2310523 /clone_end=3' /gb=AI654857 /gi=4738836 /ug=Hs.160115 /len=621
AFFX-M27830_5_at_HG-U133A			M27830 Human 28S ribosomal RNA gene, complete cds (5, _M, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)
AFFX-M27830_5_at_HG-U133B			M27830 Human 28S ribosomal RNA gene, complete cds (5, _M, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)
AFFX-M27830_M_at_HG-U133A			M27830 Human 28S ribosomal RNA gene, complete cds (5, _M, _3 represent transcript regions 5 prime, Middle, and 3 prime respectively)
AFFX-r2-Bs-dap-3_at_HG-U133A			Bacillus subtilis /REF=L38424 /DEF=B subtilis dapB, jofF, jofG genes corresponding to nucleotides 2634-3089 of L38424 /LEN=1931 (-5, -M, -3 represent transcript regions 5 prime, Middle, and 3 prime respectively)
AFFX-r2-Ec-bioD-3_at_HG-U133A			Escherichia coli /REF=J04423 /DEF=E coli bioD gene dethiobiotin synthetase corresponding to nucleotides 5312-5559 of J04423 /LEN=676 (-5 and -3 represent transcript regions 5 prime and 3 prime respectively)

Table 44

## 1007\_s\_at HG-U133A

cacccagctggtcctgtgagatgggatcctctccacccacctctagccatcccttggggaagggtggggagaaatataggatagacacigggacatggccattggag  
 5 cacctgggccccactggacaacactgattcctggacaggtggctgcgccccagcttctctccctgtcacacactggacccactggctgagaatctgggggtga  
 ggaggacaagaaggagaggaaaatgtttcctgtgctgtcctgtactgtcctcagcttggccttctcctccatcacctgaacactggacctgggggtagccc  
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 agcaacggcccatagccttgggttgacatcttagttagctgcccacattgattttctataatcactgggtttgtacattttggggggagagacacagatttttact  
 aatataatggacctagcttgaggcaat

10

## 1729\_at HG-U133A

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 agttgattgcctccccaggaggccagaccactgggggtgcatcattggggattctgcctcaggtaactttgatagagtggtgggggggggacttcttggagatcagc  
 15 ctacacttctccatccagaagcggggttacagccagccctacagtttctcactcatgaagcaccttgatcttgggtcctggacttcatcctgggtgctgcagatactg  
 cagtgaagta

## 200008\_s\_at HG-U133A

gctcgtgtaagcagctcatctgtgacccagctacgtaaaagatcgggtagaaaaagtgggccagggtgatcagagttattgcatcctcagccaccccatcaagaa  
 20 caccaatgatgccaaactcctgccagatcatttccacagaaccaagtcaatcgaaagtcagatatctacgtctgcatgatctcctttgcgcacaatgtagcagcaca  
 gggaagtacattgtatagttagtacaactgtggaaccaaggagcctgagaaggaaatcagaccagcttggagctcttggaaaccaattgaacagaaattgttag  
 catcagtgacctcctggtacaaaagacttgggaacagaaagccagatcttatttccgcacataatgatgccaccactcattttgagac

## 200008\_s\_at HG-U133B

gctcgtgtaagcagctcatctgtgacccagctacgtaaaagatcgggtagaaaaagtgggccagggtgatcagagttattgcatcctcagccaccccatcaagaa  
 25 caccaatgatgccaaactcctgccagatcatttccacagaaccaagtcaatcgaaagtcagatatctacgtctgcatgatctcctttgcgcacaatgtagcagcaca  
 gggaagtacattgtatagttagtacaactgtggaaccaaggagcctgagaaggaaatcagaccagcttggagctcttggaaaccaattgaacagaaattgttag  
 catcagtgacctcctggtacaaaagacttgggaacagaaagccagatcttatttccgcacataatgatgccaccactcattttgagac

## 30 200023\_s\_at HG-U133A

ggaggaccatgggagtgatgttcacgcctctgacagtgaaatacgcgtactacgacactgaacgcacatcgaggtgacctgatcatgaagacctgcttagccccaac  
 agagtgattggactctcaagtacttgacgaagtagggggcatcagctgcacccaggatgccctgagtacagtggtgcaatatgcagaggatgtactgtctgga  
 aagggtgcagctgacaatactgtggccgcttctgatgagcctggttaaccaaglacccgaaatagttcccgatgactttgagaccatgctcaacagcaacatcaat  
 gacctttgaltggtgacctacctggccaaacctcacacagtcacagattgcactcaatgaaaaacttgtaaacctgtgaatggacccaagcagtagactgtctgtctta  
 35 ggtattaacc

## 200040\_at HG-U133A

tgacttttcaatcgtgggttttgaatctagccccagacatactgtgtgagagatacttagagggaggaglaggtttgaagaggttgatggtggtggggagggaag  
 gcctcctgaattgagtttgatgcagagcttttagccatgaagaatcttcagtcatagtactaataataaatttcagttatataaaagacaaagtattttgctcatttgagatt  
 40 ctgcactccatgaaaagttcactggacgctggggccaaaagcgtgttatttctaagttgacggtgtgcaatatacgaaactgttcccaagtagtcaagatgtctcaac  
 actagcatgatataaaaaggacactgcagctgaatgaaaaaggaaatcaaaatccactttgtacataagttaaagtcctaatggalttgacctctccattttgttct  
 cggaagattaaatgctacatgtgtaagtctgcctaaat

## 200047\_s\_at HG-U133A

ggtttggctatctaatttgggtgtattcttgaatgtaaacacatttgtataattgtatcgtagctgattgaatcatgtagtatcaaatattagatgtagttaaagtgtaaat  
caatttaaacccattttagtcattttttccaaaaaatactgccagatgctgatgttcagtgtaattcttgcctgttcagttacagaaagggtgctcagttgtagaatgt  
attgtacctttaacacctgatgtgtacatcccatgta

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